

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 07:40:11 ; Search time 2319.58 Seconds
(without alignments)
9398.725 Million cell updates/sec

Title: US-09-864-675-3
Perfect score: 897
Sequence: 1 atgaggcgcgacccggcccc.....caatgggtcaacttctcctaa 897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*

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28:  gb_gss1:*
29:  gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

[illegible]

ALIGNMENTS

RESULT 1
 BI918620 805 bp mRNA linear EST 16-OCT-2001
 LOCUS 603176570F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240969 5',
 DEFINITION mRNA sequence.
 ACCESSION BI918620
 VERSION BI918620.1 GI:16182295
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 805)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11607 row: k column: 18
 High quality sequence start: 2
 High quality sequence stop: 778.
 FEATURES
 source Location/Qualifiers
 1. .805
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5240969"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_121"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH MGC Library."
 BASE COUNT 169 a 243 c 263 g 130 t
 ORIGIN
 Query Match 75.1%; Score 674; DB 12; Length 805;
 Best Local Similarity 98.7%; Pred. No. 4.3e-151;
 Matches 732; Conservative 0; Mismatches 5; Indels 5; Gaps 5;

QY 1 ATGAGGCGCGACCCGGCCCCCGGC-TTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTG 59
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 Db 64 ATGAGGCGCGACCCGGCCCCCGGCGTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTG 123
 QY 60 CTACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGA 119
 |||||
 Db 124 CTACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGA 183
 QY 120 GGGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCC 179
 |||||
 Db 184 GGGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCC 243
 QY 180 GCGCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGG 239
 |||||
 Db 244 GCGCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGG 303
 QY 240 GGGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCA 299
 |||||
 Db 304 GGGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCA 363
 QY 300 GCGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTG- 358
 |||||
 Db 364 GCGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGT 423
 QY 359 CCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTG 418
 |||||
 Db 424 CCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTG 483
 QY 419 ACTGCGCCACCCGGGCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGA 478
 |||||
 Db 484 ACTGCGCCACCCGGGCCAAGTTGAAGAAGATGACGAGCCAGACGGGACAGGTGGGTGAGA 543
 QY 479 AGCAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCA 538
 |||||
 Db 544 AGCAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCA 603
 QY 539 AGGATGGCAAGGAGCTCAACCG-CAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGA 597
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 Db 604 AGGATGGCAAGGAGCTCAACCGTCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGA 663
 QY 598 AAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGA-GTATGTCTG 656
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 Db 664 AAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGAGGTATGTCTG 723
 QY 657 CGAGG-CCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCG 715
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 Db 724 CGAGGCCCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGTTTTACGTCAACAGGT 783
 QY 716 TGAGCACCACCCTGTCATCCTG 737
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 Db 784 TGAGCACCAACCTGTCATCCTG 805

RESULT 2
 BM914622
 LOCUS

BM914622

1047 bp

mRNA

linear

EST 12-MAR-2002

DEFINITION AGENCOURT_6615334 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480308
5', mRNA sequence.

ACCESSION BM914622

VERSION BM914622.1 GI:19365001

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1047)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2002 row: p column: 05

High quality sequence stop: 541.

FEATURES

source

Location/Qualifiers

1..1047

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5480308"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_113"

/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT

263 a 347 c 254 g 183 t

ORIGIN

Query Match 63.1%; Score 565.6; DB 12; Length 1047;

Best Local Similarity 96.8%; Pred. No. 4.6e-125;

Matches 577; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 272 GCTCCTGTGTGCCGCTCGAAAGGAACCAGCGCTACATCTTTTTCCTGGAGCCCACGGAAC 331
|||||

Db 1 GCTCCTGTGTGCCGCTCGAAAGGAACCAGCGCTACATCTTTTTCCTGGAGCCCACGGAAC 60

Qy 332 AGCCCTTAGTCTTTAAGACGGCCTTTGCCCCCTCGATACCAACGGCAAAAATCTCAAGA 391
|||||

Db 61 AGCCCTTAGTCTTTAAGACGGCCTTTGCCCCCTCGATACCAACGGCAAAAATCTCAAGA 120

Qy 392 AAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGCCCAAGTTGAAGAAGATGA 451
|||||

Db 121 AAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGCCCAAGTTGAAGAAGATGA 180

Qy 452 AGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTA 511
 |||||

Db 181 AGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTA 240

Qy 512 ATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACA 571
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Db 241 ATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACA 300

Qy 572 TTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGG 631
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Db 301 TTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGG 360

Qy 632 TGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCC 691
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Db 361 TGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCC 420

Qy 692 GGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTTCGGGGCAGCCC 751
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Db 421 GGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTTCGGGGCAGCCC 480

Qy 752 GGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCG 811
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Db 481 GGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGCTGCTACTACATCG 540

Qy 812 AGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGT 867
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Db 541 AGGCCATCAATCAGCTTTCTGCAAATGTCCCAATGGATTCTTCCGACCAACATGT 596

RESULT 3

BI412864/c

LOCUS BI412864 1041 bp mRNA linear EST 14-AUG-2001

DEFINITION 602988202F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5144016 5', mRNA sequence.

ACCESSION BI412864

VERSION BI412864.1 GI:15173787

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1041)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

FEATURES

Location/Qualifiers

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/organism="Mus musculus"
```

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/mol type="mRNA"
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```
/strain="CZECH II"
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/db xref="taxon:10090"
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/clone="IMAGE:5144016"
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/tissue type="pooled lung tumors"
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/lab host="DH10B (phage-resistant)"
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```
/clone lib="NCI CGAP_Lu33"
```

```
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
```

modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st

strand cDNA was prepared from mRNA obtained from pooled

lung tumors with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGGAGCGCCGCTCTGTTTTTTTTTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not

I and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo. "

247 a 306 c 295 g 193 t

Query Match 52.1%; Score 467.2; DB 12; Length 1041;

Query Match 52.1%; Best Local Similarity 86.6%; Pred. No. 1.8e-101;

Best Local Similarity 86.6%; Filed NO: 1.00 101;
Matches 563; Conservative 0; Mismatches 78; Indels 9; Gaps 4;

Qy	165	CAGCACCCGAGAGCCGCCCGCCTCGGGT	CGGGT-----GGCGTTGGTAAAGGTGCTGGACA	220
Db	656	CACCTCGAGATGCCCGCCCGCCTCGGGT	CGGTTGGCGTCTTGGTGAAAGGTGCTGGACA	597
Qy	221	AGTGGCCG--CTCCGGAGCGGGGGGCTGCAGCG	GAGCAGGTGATCAGCGTGGGGCTCCTG	278
Db	596	AGTTGCCGGCTCCCGGATCGGGGGGCTGCAGCG	GAGCAGGTGATCAGCGTGGGGCTCCTG	537
Qy	279	TGTGCCGCTCGAAAGGAACCAGCGCTACATCTT	-TTTCCTGGAGCCACGGAACAGCCCT	337
Db	536	TGCGCCGCTCGAAAGGAACCAGCGCTACATCTT	GTTCCTGGAGCCACCGAGCAGCCCT	477
Qy	338	TAGTCTTTAAGACGGCCTTTGCCCCCTCGATA	CCAAACGGCAAAAATCTCAAGAAAGAGG	397
Db	476	TAGTTTTTAAGACAGCCTTTTGCCCCGGTCG	ACCCTACGGCAAATACATCAAGAAAGAGG	417
Qy	398	TGGGCAAGATCCTGTGCACTGACTGCGCCAC	CCGGCCCAAGTTGAAGAAGATGAAGAGCC	457
Db	416	TGGGCAAGATCCTGTGCACTGACTGCGCCAC	CCGGCCCAAGCTGAAGAAGATGAAGAGCC	357
Qy	458	AGACGGGACAGGTGGGTGAGAAGCAATCGCT	GAAAGTGTGAGGCAGCAGCCGTAATCCCC	517
Db	356	AGACAGGAGAGGTGGGTGAGAAGCAGTCGCT	CAAGTGTGAGGCAGCGGCGGGAACCCCC	297
Qy	518	AGCCTTCCTACCGTTGGTTCAAGGATGGCA	AAGGAGCTCAACCGCAGCCGAGACATTCGCA	577
Db	296	AGCCCTCCTATCGCTGGTTCAAGGATGGCA	AAGGAAGTCAACCGGAGTCGTGATATTCGCA	237

Qy 578 TCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGG 637
 |||| ||||||| ||||||||||||||| ||||||||||||| |||| |||||||
 Db 236 TCAAGTATGGCAATGGCAGAAAGAACTCACGGCTACAGTTCAACAAAGTGAGGGTGGAGG 177
 Qy 638 ACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCC 697
 | || ||||||| |||| ||||||||||||||| ||||||||||||| |||||||
 Db 176 ATGCCGGGGAGTACGTCTGTGAGGCCGAGAACATCCTTGGGAAGGACACCGTGAGGGGCC 117
 Qy 698 GGCTTTACGTCAACAGCGTGAGCACCACCCTGTTCATCCTGGTTCGGGGCACGCCCCGGAAGT 757
 | || | ||||||||||||||||||| ||||||||||||| || |||||||||
 Db 116 GACTCCATGTCAACAGCGTGAGCACCCTGTTCATCCTGGTTCGGGACATGCCCGGAAGT 57
 Qy 758 GCAACGAGACAGCCAAGTCCTA--TTGCGTCAATGGAGGCGTCTGCTACT 805
 |||| ||||| ||||||||||| || || ||||||||||| |||||||
 Db 56 GCAATGAGACCGCCAAGTCCTACCATGTGTGAATGGAGGCGTGTGCTACT 7

RESULT 4

BX281777

LOCUS BX281777 524 bp mRNA linear EST 04-MAR-2003

DEFINITION BX281777 NIH_MGC_121 Homo sapiens cDNA clone IMAGp998K1811607 ;
 IMAGE:5240969, mRNA sequence.

ACCESSION BX281777

VERSION BX281777.1 GI:28612804

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 524)

AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
 Radelof,U., Schneider,D. and Korn,B.

TITLE Human UnigeneSet - RZPD3

JOURNAL Unpublished

COMMENT Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGp998K1811607.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human UnigeneSet - RZPD3 (RZPDLIB No.972)

[http://www.rzpd.de/CloneCards/cgi-](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972)

[bin/showLib.pl.cgi/response?libNo=972](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972) Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT.

FEATURES

source

Location/Qualifiers

1. .524

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGp998K1811607 ; IMAGE:5240969"


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/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH MGC Library."

```

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BASE COUNT      99 a      174 c      172 g      79 t
ORIGIN

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Query Match          52.1%; Score 467; DB 13; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.6e-101;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
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Db      58 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 117

Qy      61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        |||
Db     118 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 177

Qy     121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
        |||
Db     178 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 237

Qy     181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
        |||
Db     238 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 297

Qy     241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
        |||
Db     298 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 357

Qy     301 CGCTACATCTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
        |||
Db     358 CGCTACATCTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 417

Qy     361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
        |||
Db     418 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 477

Qy     421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACA 467
        |||
Db     478 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACA 524

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RESULT 5

AA706226

```

LOCUS      AA706226          549 bp      mRNA      linear      EST 12-JAN-1999
DEFINITION ah28a07.s1 Soares_parathyroid tumor NbHPA Homo sapiens cDNA clone
            1240116 3' similar to TR:P43328 P43328 NEU DIFFERENTIATION FACTOR

```

NDF04 ;, mRNA sequence.

ACCESSION AA706226

VERSION AA706226.1 GI:2716144

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 549)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Insert Length: 689 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 451.

FEATURES

source Location/Qualifiers

1. .549
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1240116"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer
[5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT
TTTTT-3'], double-stranded cDNA was size selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

BASE COUNT 137 a 163 c 156 g 92 t 1 others

ORIGIN

Query Match 45.5%; Score 408.2; DB 9; Length 549;
Best Local Similarity 91.7%; Pred. No. 2.1e-87;

Matches 431; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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Qy      424 GCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 483
          |||
Db      15  GCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 74

Qy      484 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 543
          |||
Db      75  TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 134

Qy      544 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAAC 603
          |||
Db      135 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAAC 194

Qy      604 TCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCC 663
          |||
Db      195 TCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCC 254

Qy      664 GAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACC 723
          |||
Db      255 GAGAACATCCTGGGGAAGGACACCGTCCGGAGGCCGGCTTTACGTCAACAGCGTGAGCACC 314

Qy      724 ACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGC 783
          |||
Db      315 ACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGNGACAGCCAAGTCCTATTGC 374

Qy      784 GTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCCCT 843
          |||
Db      375 GTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGGCACCT 434

Qy      844 GTGGGATACACCGGGGACAGGTGTGAGCAGTTCGCAATGGTCAACTTCTC 893
          || || || || || || || || || ||
Db      435 GGGCTGCACTGCTTAGAAGTTGGTACCCAGAGCCACCACTTCCCCATCTC 484

```

RESULT 6

AI041451

LOCUS AI041451 412 bp mRNA linear EST 28-AUG-1998

DEFINITION ow36c02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
IMAGE:1648898 3' similar to TR:014511 014511 NTAK. ;, mRNA
sequence.

ACCESSION AI041451

VERSION AI041451.1 GI:3280645

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 412)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo,
Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 671 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source Location/Qualifiers
1. .412
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1648898"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia)
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer
[5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT
TTTTT-3'], double-stranded cDNA was size selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

BASE COUNT 112 a 108 c 126 g 65 t 1 others
ORIGIN

Query Match 44.2%; Score 396.6; DB 9; Length 412;
Best Local Similarity 97.6%; Pred. No. 1.2e-84;
Matches 402; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy	426	CACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATC	485
Db	1	CACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATC	60
Qy	486	GCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGG	545
Db	61	GCTGAAGTGTGAGGCAGCAGCGATAAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGG	120
Qy	546	CAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAACTC	605
Db	121	CAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAACTC	180
Qy	606	ACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGA	665
Db	181	ACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGA	240

BASE COUNT	114 a	112 c	145 g	56 t
ORIGIN				

QY	363	CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG	422
Db	5	CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA	64
QY	423	CGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	482
Db	65	AGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	124
QY	483	ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	542
Db	125	ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	184
QY	543	TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA	602
Db	185	TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA	244
QY	603	CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	662
Db	245	CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	304
QY	663	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	722
Db	305	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	364
QY	723	CACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG	782
Db	365	CACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG	424
QY	783	CGT	785
Db	425	CGT	427

XX

KW EST; expressed sequence tag.
XX
OS Mus musculus (house mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
XX

RN [1]
RP 1-488
RA Heil O., Ebert L., Neubert P., Peters M., Radelof U., Schneider D.,
RA Korn B.;
RT ;
RL Submitted (28-MAY-2003) to the EMBL/GenBank/DDBJ databases.
RL RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer
RL Feld 580, D-69120 Heidelberg, Germany
XX

CC RZPD; IMAGp998N017639.
CC RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
CC Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
CC <http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=981>
CC Contact: Ina Rolfs
CC RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
CC Heubnerweg 6, D-14059 Berlin, Germany
CC Tel: +49 30 32639 101
CC Fax: +49 30 32639 111
CC www.rzpd.de
CC This clone is available royalty-free from RZPD;
CC contact RZPD (clone@rzpd.de) for further information.
CC Seq primer: SP6, Primer sequence: ATTTAGGTGACACTATAG
XX

FH Key	Location/Qualifiers
FT source	1. .488
FT	/db_xref="taxon:10090"
FT	/note="Cloned unidirectionally. Primer: Oligo dT. Average
FT	insert 2 kb. Library constructed by Life Technologies,
FT	catalog #12017-018. Investigators providing samples: Lothar
FT	Hennighausen/Chu-Xia Deng, NIH Reference for transgenic
FT	model: Xu et al., Nature Genetics 22, 37-43 (1999). Note:
FT	this is a NCI_CGAP Library
FT	< http://www.ncbi.nlm.nih.gov/ncicgap/ >."
FT	/organism="Mus musculus"
FT	/clone="IMAGp998N017639"
FT	/clone_lib="NCI_CGAP_Mam3 mammary tumor"
FT	/lab_host="DH10B"

XX
SQ Sequence 488 BP; 129 A; 116 C; 149 G; 94 T; 0 other;
Query Match 35.5%; Score 318.6; DB 4; Length 488;
Best Local Similarity 86.7%; Pred. No. 6.1e-66;
Matches 351; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY	469	GTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGAATCCCCAGCCTTCCTAC	528
Db	1	GTGGGTGAGAAGCAGTCGCTCAAGTGTGAGGCAGCGCGGGAACCCCCAGCCCTCCTAT	60
QY	529	CGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGC	588

Db	61	CGCTGGTTCAAGGATGGCAAGGAACTCAACCGGAGTCGTGATATTTCGCATCAAGTATGGC	120
QY	589	AACGGCAGAAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAG	648
Db	121	AATGGCAGAAAAGAACTCACGGCTACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAG	180
QY	649	TATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTC	708
Db	181	TACGTCTGTGAGGCCGAGAACATCCTTGGAAGGACACCGTGAGGGGCCGACTCCATGTC	240
QY	709	AACAGCGTGAGCACCACCCTGTTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACA	768
Db	241	AACAGCGTGAGCACCCTGTTCATCCTGGTCGGGGACATGCCCGGAAGTGCAATGAGACC	300
QY	769	GCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTC	828
Db	301	GCCAAGTCCTACTGTGTGAATGGAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTC	360
QY	829	TCCTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGTTCAGCAG	873
Db	361	TCCTGCAAATGTCCAAACGGATTCTTCGGACAGAGATGTTTGGAG	405

RESULT 9

BI410828/c

LOCUS

BI410828

949 bp

mRNA

linear

EST 14-AUG-2001

DEFINITION

00298373411 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5119065 5',
mRNA sequence.

mRNA sequence.

ACCESSION

BI410828

VERSION

BI410828.1 GI:15171751

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 949)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11290 row: d column: 10

High quality sequence start: 28

High quality sequence stop: 919.

FEATURES

Location/Qualifiers

source

1. .949

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/organism="Mus musculus"
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/mol type="mRNA"
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/strain="CZECH TT"
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/db_xref="taxon:10090"
 /clone="IMAGE:5119065"
 /tissue_type="pooled lung tumors"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NCI_CGAP_Lu33"
 /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5' TGTACCAATCTGAAGTGGGAGCGGCCGCCTCTGTTTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 171 a 261 c 269 g 248 t
 ORIGIN

Query Match 28.4%; Score 255; DB 12; Length 949;
 Best Local Similarity 80.0%; Pred. No. 1.3e-50;
 Matches 388; Conservative 0; Mismatches 85; Indels 12; Gaps 7;

QY	397	GTGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGC	456
Db	947	GTGGGCCAGATCCTGGGCACTG-CTGCGCCACCCGCCCCAA-CTGAAGAAGATGAAGA-C	891
QY	457	CAGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCC	516
Db	890	CAAACCAGAAGAGTCGGTGAGAACAGTTCGCTCAAGTGTGAGGCACGGCCGGGGAAACCC	831
QY	517	CAGCCTTCCTACC-----GTTGGTTCAAGGATGGC-AAGGAGCTCAACCGCAGCCGAGAC	570
Db	830	CCCCACCCCTCCCTATCGCTGGTTTCAAGGATGGCAAAGGAAGTCAACCGGAGTCGTGAT	771
QY	571	ATTTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAG	630
Db	770	ATTTCGCATCAAGTATGCCAATGGCAGAAAGAACTCACGGCTACAGTTCAACAAAAGTGAG	711
QY	631	GT--GGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCG	688
Db	710	GTTGGAGGATTGCCGGGGAGTACGTCTGTGAGGCCGAGAACATCCTTGGGAAGGACACCG	651
QY	689	TCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTTCATCCTGGTCGGGGCAGC	748
Db	650	T-GAGGGCCGACTCCATGTCAACAGCGTGAGCACCCTGTTCATCCTGGTCGGGGACATG	592
QY	749	CCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACA	808
Db	591	CCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATGGAGGCGTGTGCTACTACA	532
QY	809	TCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGTC	868
Db	531	TCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGATTCTTCGGACAGAGATGTT	472
QY	869	AGCAG	873
Db	471	TGGAG	467

RESULT 10
 BE983573
 LOCUS BE983573 333 bp mRNA linear EST 29-APR-2002
 DEFINITION UI-M-CG0p-bgi-c-07-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
 UI-M-CG0p-bgi-c-07-0-UI 3', mRNA sequence.
 ACCESSION BE983573
 VERSION BE983573.1 GI:10654893
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 333)
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mEST@mail.nih.gov
 Oligo-dT track not found, Not I site shown in beginning of sequence
 is likely internal to the message. cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
 clones from RESEARCH GENETICS. It should be noted that Bento Soares
 is generating a small number of additional specialized
 non-redundant arrays of BMAP cDNAs whose availability will be
 considered under appropriate and limited collaborative arrangements
 The tissue for this library was contributed by Dr. Xin-Yuan Fu,
 Yale University School of Medicine The following repetitive
 elements were found in this cDNA sequence: 15-105,
 >GC_rich#Low_complexity
 Seq primer: M13 Forward
 POLYA=No.
 FEATURES
 source Location/Qualifiers
 1. .333
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-CG0p-bgi-c-07-0-UI"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NIH_BMAP_Ret4_S2"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The
 NIH_BMAP_Ret4_S2 library is a subtracted library,
 ultimately derived from mouse retina tissue libraries at
 various stages of development. For a detailed description
 of the library from which this clone was derived, please
 visit our web site at brainest.eng.uiowa.edu. The tissue

for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine

TAG_SEQ=None found"

BASE COUNT 47 a 124 c 122 g 40 t
ORIGIN

Query Match 26.1%; Score 234.4; DB 10; Length 333;
Best Local Similarity 95.6%; Pred. No. 8.4e-46;
Matches 241; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCTCGCTCGCCTGC 60
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Db      82 ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 141
      |||
QY      61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
      |||
Db     142 TACTCGCCAGCCTCAAGTCGGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 201
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QY     121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
      |||
Db     202 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCG 261
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QY     181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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Db     262 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 321
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QY     241 GGGCTGCAGCGC 252
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Db     322 GGGCTGCAGCGC 333
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RESULT 11

AA772412

LOCUS

AA772412

297 bp

mRNA

linear

EST 31-DEC-1998

DEFINITION

ai44e12.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
1359886 3' similar to TR:P43328 P43328 NEU DIFFERENTIATION FACTOR
NDF04 ;, mRNA sequence.

ACCESSION

AA772412

VERSION

AA772412.1 GI:2824195

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 297)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Insert Length: 667 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 267.

source

1. 297

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/dev_stage="adult"
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/clone_lib="Soares_parathyroid_tumor NbHPA"
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/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer

```

[5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT
TTTTT-3'], double-stranded cDNA was size selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

BASE COUNT
ORIGIN

87 a 68 c 105 g 37 t

Query Match

25.0%; Score 224; DB 9; Length 297;

Best Local Similarity 92.2%; Pred. No. 2.5e-43;
Matches 236;

Matches 236; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 405 GATCCTGTGCACTGACTGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGG 464

Db
42 GAGCCCGATCCCGGGAGAAAGCCACCCGGCCAAGTTGAAGAAGATGAAGAGCCAGACGGG 101

QY 465 ACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTC 524

Db
102 ACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCGGTGAATCCCCAGCCTTC 161

Qy 525 CTACCGTTGGTTC AAGGATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATA 584

Db 162 CTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATA 221

Qy 585 TGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGG 644

Db 222 TGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGG 281

Qy 645 GGAGTATGTCTGCGAG 660

Db 282 GGAGTATGTCTGCGAG 297

RESULT 12

BI651936

LOCUS

BI651936

795 bp

mRNA

linear

EST 12-SEP-2001

DEFINITION

603298677F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5339251 5', mRNA sequence.

ACCESSION

BI651936

VERSION

BI651936.1 GI:15566172

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 795)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11861 row: j column: 20

High quality sequence stop: 795.

FEATURES

source

Location/Qualifiers

1. .795

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5339251"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Mam3"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

Reference for transgenic model: Xu et al., Nature Genetics

22, 37-43 (1999)."

BASE COUNT

204 a 226 c 219 g 146 t

ORIGIN

Query Match

23.4%; Score 210.2; DB 12; Length 795;

Best Local Similarity 86.2%; Pred. No. 7e-40;

Matches 244; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

QY

592 GGCAGAAAGAACTCACGAC-TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTA 650

Db

1 GGCAGAAAGAACTCACGGCTTACAGTTCAACAAGGTGAGGGTGGAGGATGCCGGGGAGTA 60

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 07:12:21 ; Search time 3588 Seconds
(without alignments)
10227.407 Million cell updates/sec

Title: US-09-864-675-3

Perfect score: 897

Sequence: 1 atgaggcgcgacccggcccc.....caatgggtcaacttctcctaa 897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
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- 26: em_ro:*
- 27: em_sts:*

28: em_un:*
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 32: em_htg_other:*
 33: em_htg_mus:*
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 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	849	94.6	3020	9	AB005060		
2	835.4	93.1	1884	6	AR098145		AB005060 Homo sapi
3	835.4	93.1	1884	6	AR116617		AR098145 Sequence
4	784	87.4	3441	6	AR072052		AR116617 Sequence
5	738.6	82.3	993	6	AR072053		AR072052 Sequence
6	737	82.2	2947	10	D89995		AR072053 Sequence
7	737	82.2	3076	6	E16456		D89995 Rattus sp.
8	737	82.2	3077	10	D89996		E16456 Rat mRNA fo
9	427.8	47.7	1476	6	AR098146		D89996 Rattus sp.
10	427.8	47.7	1476	6	AR116618		AR098146 Sequence
11	427.8	47.7	2268	6	AR098155		AR116618 Sequence
12	427.8	47.7	2268	6	AR116627		AR098155 Sequence
13	425	47.4	2188	10	AB001576		AR116627 Sequence
14	424.8	47.4	118504	9	AC094080		AB001576 Rattus sp
c 15	424.8	47.4	152838	2	AC011589		AC094080 Homo sapi
16	424.8	47.4	170797	9	AC011379		AC011589 Homo sapi
17	424.8	47.4	210675	2	AC026272		AC011379 Homo sapi
18	424	47.3	1054	6	AX406616		AC026272 Homo sapi
19	424	47.3	1054	9	HS2NRG01		AX406616 Sequence
20	405.4	45.2	1607	6	AR098144		AF119151 Homo sapi
21	405.4	45.2	1607	6	AR116616		AR098144 Sequence
22	405.4	45.2	2467	6	AR098143		AR116616 Sequence
23	405.4	45.2	2467	6	AR116615		AR098143 Sequence
24	387.2	43.2	140307	2	AC131191		AR116615 Sequence
25	384	42.8	253462	2	AC096477		AC131191 Mus muscu
26	216.2	24.1	1207	6	AR072054		AC096477 Rattus no
27	173	19.3	419	6	AX406617		AR072054 Sequence
28	173	19.3	419	9	HS2NRG02		AX406617 Sequence
29	173	19.3	120236	9	AC008523		AF119152 Homo sapi
c 30	173	19.3	189050	9	AC008667		AC008523 Homo sapi
31	142.6	15.9	85703	2	AC020830		AC008667 Homo sapi
c 32	142.6	15.9	191101	2	AC127350		AC020830 Mus muscu
33	139.4	15.5	226038	2	AC106592		AC127350 Mus muscu
							AC106592 Rattus no

	34	139.4	15.5	273080	2	AC098540	AC098540 Rattus no
c	35	139.4	15.5	302176	2	AC096479	AC096479 Rattus no
	36	130.2	14.5	163	10	AY227026	AY227026 Mus muscu
	37	124.6	13.9	493	6	AX406618	AX406618 Sequence
	38	124.6	13.9	493	9	HS2NRG03	AF119153 Homo sapi
	39	124	13.8	350	6	AX406619	AX406619 Sequence
	40	124	13.8	350	9	HS2NRG04	AF119154 Homo sapi
c	41	109.6	12.2	85703	2	AC020830	AC020830 Mus muscu
	42	108.4	12.1	206683	2	BX323592	BX323592 Danio rer
	43	108.4	12.1	220700	2	BX005008	BX005008 Danio rer
	44	97	10.8	172	10	D89997	D89997 Rattus sp.
	45	84.8	9.5	240	10	AY227025	AY227025 Mus muscu

ALIGNMENTS

RESULT 1
AB005060

LOCUS AB005060 3020 bp mRNA linear PRI 14-NOV-1997

DEFINITION Homo sapiens mRNA for NTAK, complete cds.

ACCESSION AB005060

VERSION AB005060.1 GI:2626738

KEYWORDS NTAK.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Higashiyama, S., Horikawa, M., Yamada, K., Ichino, N., Nakano, N., Nakagawa, T., Miyagawa, J., Matsushita, N., Nagatsu, T., Taniguchi, N. and Ishiguro, H.

TITLE A novel brain-derived member of the epidermal growth factor family that interacts with ErbB3 and ErbB4

JOURNAL J. Biochem. 122 (3), 675-680 (1997)

MEDLINE 98006324

PUBMED 9348101

REFERENCE 2 (bases 1 to 3020)

AUTHORS Ishiguro, H.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-1997) Hiroshi Ishiguro, Fujita Health University, ICMS; 1-98, kutsukake-cho, Toyoake, Aichi 470-11, Japan (E-mail:hishi@fujita-hu.ac.jp, Tel:0562-93-9393, Fax:0562-93-8831)

FEATURES

source Location/Qualifiers

1. .3020
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="SK-N-SH"
/cell_type="neuroblastoma"

CDS 226. .2778
/codon_start=1
/product="NTAK"
/protein_id="BAA23417.1"
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/translation="MRQVCCSALPPPPLEKGRCSSYSDSSSSSSERSSSSSSSSSESG
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KNLKKEVGKILCTDCATRPKLKKMKSQTGQVGEKQSLKCEAAAGNPQPSYRWFKDGKE
LNRSRDIRIKYGNRKNRSRLQFNKVVEDAGEYVCEAENILGKDTVGRGLYVNSVSTT
LSSWSGHARKCNETAKSYCVNGGVCYYIEGINQLSCKCPNGFFGQRCLEKLPLRLYMP
DPKQKAEELYQKRVLTITGICVALLVVGIVCVVAYCKTKKQKQMHNLHRLQNMCPAHQ
NRSLANGPSPHRLDPEEIOMADYISKNPATDHVIRRETETTFSGSHSCSPSHHCSTA
TPTSSHRHESHTWSLSESLTSDSQSGIMLSSVGTSKCNSPACVEARARRAAAYNLE
ERRRATAPPYHDSVDSLSDSPHSERYVSALTTPARLSPVDFHYSLATQVPTFEITSPN
SAHAVSLPPAAPISYRLAEQQPLLRRHPAPPGPGPGPGADMQRSYDSYYPAA
GPGPRRGTCALGGSGLSLPASFPRIPEDEYETTQECAPPPPRPRARGASRRTSAGP
RRWRRSRLNGLAAQRARAARDSLSLSSGSGGGSASASDDDDADDAGALAAESTPFLGL
RGAHDALRSDSPPLCPAADSRTYYSLDSHSTRASSRHSRGPppPRAKQDSAPL"

polyA_site

3020

/note="39 A nucleotides"

BASE COUNT 615 a 1015 c 937 g 453 t
ORIGIN

Query Match 94.6%; Score 849; DB 9; Length 3020;
Best Local Similarity 98.3%; Pred. No. 7.3e-152;
Matches 858; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC	60
Db	502	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC	561
Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	562	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	621
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	622	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	681
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	682	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	741
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	742	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	801
Qy	301	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	802	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	861
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	862	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	921
Qy	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	922	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	981
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	982	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	1041

QY 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG 600
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 Db 1042 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG 1101
 QY 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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 Db 1102 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 1161
 QY 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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 Db 1162 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 1221
 QY 721 ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
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 Db 1222 ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 1281
 QY 781 TGGCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
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 Db 1282 TGGCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 1341
 QY 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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 Db 1342 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 1374

RESULT 2

AR098145
 LOCUS AR098145 1884 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 5 from patent US 6074841.
 ACCESSION AR098145
 VERSION AR098145.1 GI:12807402
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1884)
 AUTHORS Gearing,D.P. and Busfield,S.J.
 TITLE Don-1 gene and polypeptides and uses therefor
 JOURNAL Patent: US 6074841-A 5 13-JUN-2000;
 FEATURES Location/Qualifiers
 source 1. .1884
 /organism="unknown"
 BASE COUNT 426 a 607 c 560 g 291 t
 ORIGIN

Query Match 93.1%; Score 835.4; DB 6; Length 1884;
 Best Local Similarity 98.1%; Pred. No. 2.9e-149;
 Matches 856; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC 60
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 Db 218 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC 277
 QY 61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
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 Db 278 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 337

QY 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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 Db 338 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 397

QY 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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 Db 398 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 457

QY 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
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 Db 458 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 517

QY 301 CGCTACATCTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
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 Db 518 CGCTACATCTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 577

QY 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
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 Db 578 CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC 636

QY 421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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 Db 637 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 696

QY 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
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 Db 697 CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 756

QY 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG 600
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 Db 757 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG 816

QY 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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 Db 817 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 876

QY 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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 Db 877 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 936

QY 721 ACCACCCTGTCATCCTGGTCCGGGACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
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 Db 937 ACCACCCTGTCATCCTGGTCCGGGACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 996

QY 781 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
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QY 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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 Db 1057 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 1089

RESULT 3
 AR116617
 LOCUS

AR116617

1884 bp

DNA

linear

PAT 16-MAY-2001

DEFINITION Sequence 5 from patent US 6133423.
 ACCESSION AR116617
 VERSION AR116617.1 GI:14096939
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1884)
 AUTHORS Gearing,D.P. and Busfield,S.J.
 TITLE Don-1 gene and polypeptides and uses therefor
 JOURNAL Patent: US 6133423-A 5 17-OCT-2000;
 FEATURES Location/Qualifiers
 source 1. .1884
 /organism="unknown"
 BASE COUNT 426 a 607 c 560 g 291 t
 ORIGIN

Query Match 93.1%; Score 835.4; DB 6; Length 1884;
 Best Local Similarity 98.1%; Pred. No. 2.9e-149;
 Matches 856; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	60
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Qy	61	TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	278	TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	337
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	338	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	397
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	398	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	457
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	458	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	517
Qy	301	CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	518	CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	577
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	578	CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC	636
Qy	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	637	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	696
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	697	CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	756

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Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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 Db 817 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 876

Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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 Db 877 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 936

Qy 721 ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
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 Db 937 ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 996

Qy 781 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
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RESULT 4

AR072052

LOCUS AR072052 3441 bp DNA linear PAT 18-FEB-2000

DEFINITION Sequence 1 from patent US 5912326.

ACCESSION AR072052

VERSION AR072052.1 GI:7222940

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 3441)

AUTHORS Chang,H.

TITLE Cerebellum-derived growth factors

JOURNAL Patent: US 5912326-A 1 15-JUN-1999;

FEATURES Location/Qualifiers

source 1. .3441

/organism="unknown"

BASE COUNT 777 a 1057 c 1015 g 592 t

ORIGIN

Query Match 87.4%; Score 784; DB 6; Length 3441;

Best Local Similarity 92.2%; Pred. No. 1.8e-139;

Matches 826; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC 60
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 Db 180 ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 239

Qy 61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
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 Db 240 TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 299

Qy 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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 Db 300 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCAGCTCTAACAGCACCCGAGAGCCT 359
 Qy 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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 Db 360 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 419
 Qy 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
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 Db 420 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 479
 Qy 301 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
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 Db 480 CGCTACATCTTTTTCCTGGAGCCCACCGAGCAGCCCTTAGTCTTTAAGACAGCCTTTGCC 539
 Qy 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
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 Db 540 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 599
 Qy 421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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 Db 600 TGCGCAACCCGGCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 659
 Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
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 Db 660 CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCCAGCCCTCCTATCGATGGTTCAAG 719
 Qy 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAAG 600
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 Db 720 GACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGCATCAAGTATGGCAACGGCAGAAAAG 779
 Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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 Db 780 AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG 839
 Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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 Db 840 GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC 899
 Qy 721 ACCACCCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
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 Db 900 ACCACTCTGTCGTCTGGTTCGGGGCACGCCCCGGAAGTGCAATGAGACAGCCAAGTCCTAC 959
 Qy 781 TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
 || |||||
 Db 960 TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAGTGT 1019
 Qy 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTCCTA 896
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 Db 1020 CCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTCAA 1075

RESULT 5

AR072053

LOCUS AR072053 993 bp DNA linear PAT 18-FEB-2000
 DEFINITION Sequence 3 from patent US 5912326.

ACCESSION AR072053
 VERSION AR072053.1 GI:7222941
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 993)
 AUTHORS Chang,H.
 TITLE Cerebellum-derived growth factors
 JOURNAL Patent: US 5912326-A 3 15-JUN-1999;
 FEATURES Location/Qualifiers
 source 1. .993
 /organism="unknown"
 BASE COUNT 230 a 271 c 311 g 181 t
 ORIGIN

Query Match 82.3%; Score 738.6; DB 6; Length 993;
 Best Local Similarity 90.4%; Pred. No. 8.6e-131;
 Matches 789; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC	60
Db	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC	60
Qy	61	TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	61	TACTCGCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	121	GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT	180
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	181	CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG	300
Qy	301	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	301	CGCTACATCTTTTTCCTGGAGCCACCGAGCAGCCCTTAGTTTTTAAGACAGCCTTTGCC	360
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	361	CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Qy	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	421	TGCGCAACCCGGCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG	480
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	481	CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCCAGCCCTCCTATCGATGGTTCAAG	540
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG	600

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Db      541 GACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGCATCAAGTATGGCAACGGCAGAAAG 600
QY      601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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Db      601 AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG 660
QY      661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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Db      661 GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC 720
QY      721 ACCACCCTGTCATCCTGGTCTGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
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Db      721 ACCACTCTGTCTGTCCTGGTCTGGGGCACGCCCCGGAAGTGCAATGAGACAGCCAAGTCCTAC 780
QY      781 TGCCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCGAGCTCTCCTGCAAGTGT 840
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Db      781 TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGT 840
QY      841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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RESULT 6

D89995

LOCUS D89995 2947 bp mRNA linear ROD 07-FEB-1999

DEFINITION Rattus sp. mRNA for NTAK alphas, complete cds.

ACCESSION D89995

VERSION D89995.1 GI:2605629

KEYWORDS NTAK alphas.

SOURCE Rattus sp.

ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (sites)

AUTHORS Higashiyama,S., Horikawa,M., Yamada,K., Ichino,N., Nakano,N.,
Nakagawa,T., Miyagawa,J., Matsushita,N., Nagatsu,T., Taniguchi,N.
and Ishiguro,H.

TITLE A novel brain-derived member of the epidermal growth factor family
that interacts with ErbB3 and ErbB4

JOURNAL J. Biochem. 122 (3), 675-680 (1997)

MEDLINE 98006324

PUBMED 9348101

REFERENCE 2 (bases 1 to 2947)

AUTHORS Ishiguro,H.

TITLE Direct Submission

JOURNAL Submitted (21-DEC-1996) Hiroshi Ishiguro, Fujita Health University,
ICMS; 1-98, kutsukake-cho, Toyoake, Aichi 470-11, Japan
(E-mail:hishi@fujita-hu.ac.jp, Tel:0562-93-9393, Fax:0562-93-8831)

COMMENT Sequence updated (28-Feb-1997) by:Hiroshi Ishiguro.

FEATURES Location/Qualifiers

source 1. .2947
/organism="Rattus sp."
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/db_xref="taxon:10118"

CDS

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BASE COUNT 665 a 945 c 895 g 442 t
ORIGIN

Query Match 82.2%; Score 737; DB 10; Length 2947;
Best Local Similarity 90.3%; Pred. No. 1.6e-130;
Matches 788; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC	60
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Qy	61	TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	463	TACTCGCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	522
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	523	GGCAAGGTACAGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT	582
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	583	CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	642
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	643	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG	702
Qy	301	CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	703	CGCTACATCTTTTTCCTGGAGCCCACCGAGCAGCCCTTAGTTTTTAAGACAGCCTTTGCC	762
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	763	CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	822

Qy	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	823	TGCGCAACCCGGCCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG	882
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	883	CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCAGCCCTCCTATCGATGGTTCAAG	942
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	943	GACGGCAAGGAGCTCAACCGGAGTCGTGACATTCGCATCAAGTATGGCAACGGCAGAAAG	1002
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	1003	AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG	1062
Qy	661	GCCGAGAACATCCTTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	1063	GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC	1122
Qy	721	ACCACCTGTTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	1123	ACCACCTGTGTCGTCTGGTCGGGGCACGCCCGGAAGTGCAATGAGACAGCCAAGTCCTAC	1182
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Db	1183	TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGT	1242
Qy	841	CCTGTGGGATACACCGGGGACAGGTGTCAGCAG	873
Db	1243	CCAAACGGATTCTTCGGACAGAGATGTTTGGAG	1275

E16456

VERSION E16456.1 GI:5711139

SOURCE Rattus sp.

ORGANISM *Rattus* sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 3076)

AUTHORS Higashiyama, S., Taniguchi, N., Ishiguro, K. and Nagatsu, T.

TITLE GENE ENCODING RECEPTOR TYPE TYROSINE-KINASE ERB B LIGAND AND ITS

JOURNAL Patent: JP 1998179166-A 1 07-JUL-1998;

HIGASHIYAMA SHIGEKI

COMMENT	OS	Rattus sp. (rat)
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PN JP 1998179166-A/1

PD 07-JUL-1998

PF 25-DEC-1996 JP 1996356998

PI HIGASHIYAMA SHIGEKI, TANIGUCHI NAOYUKI, ISHIGURO KEIJI, PI

NAGATSU TOSHIHARU

PC C12N15/09,C07K14/705,C07K16/28,C12N5/10,C12N15/02,C12P21/02,
 PC C12P21/08,
 PC C12Q1/68,G01N33/53,G01N33/566//A61K31/70,A61K38/46,A61K39/395,
 PC A61K48/00,
 PC C07H21/04,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91); CC
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 CC topology: Linear;
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 FT source 1. .3076
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FEATURES Location/Qualifiers
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BASE COUNT 673 a 996 c 944 g 463 t
 ORIGIN

Query Match 82.2%; Score 737; DB 6; Length 3076;
 Best Local Similarity 90.3%; Pred. No. 1.6e-130;
 Matches 788; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
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 Db 556 ATGAGGCGCGACCCGGCCCCCGGCTCCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 615
 Qy 61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
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 Db 616 TACTCGCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 675
 Qy 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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 Db 676 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCAGCTCTAACAGCACCCGAGAGCCT 735
 Qy 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGCCGCTCCGGAGCGGG 240
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 Db 736 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGCCGCTCCGGAGCGGG 795
 Qy 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
 ||||||||||||||| ||||||||||||||| | |||||||||||
 Db 796 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 855
 Qy 301 CGCTACATCTTTTCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
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 Db 856 CGCTACATCTTTTCTGGAGCCCACCGAGCAGCCCTTAGTCTTTAAGACAGCCTTTGCC 915
 Qy 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
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 Db 916 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 975
 Qy 421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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Db	976	TGCGCAACCCGGCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG	1035
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Db	1036	CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCAGCCCTCTATCGATGGTTCAAG	1095
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	1096	GACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGCATCAAGTATGGCAACGGCAGAAAG	1155
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	1156	AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG	1215
Qy	661	GCCGAGAACATCCTTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	1216	GCTGAGAACATCCTTGGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC	1275
Qy	721	ACCACCCTGTCATCCTGGTTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	1276	ACCACTCTGTCTCCTGGTTCGGGGCACGCCCGGAAGTGCAATGAGACAGCCAAGTCCTAC	1335
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Db	1336	TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGT	1395
Qy	841	CCTGTGGGATACACCGGGGACAGGTGTCAGCAG	873
Db	1396	CCAAACGGATTCTTTCGGACAGAGATGTTTGGAG	1428

(E-mail:hishi@fujita-hu.ac.jp, Tel:0562-93-9393, Fax:0562-93-8831)

FEATURES

source

Location/Qualifiers

1. .3077

/organism="Rattus sp."

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BASE COUNT 673 a 996 c 945 g 463 t
ORIGIN

Query Match 82.2%; Score 737; DB 10; Length 3077;
Best Local Similarity 90.3%; Pred. No. 1.6e-130;
Matches 788; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC 60
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Db 557 ATGAGGCGCGACCCGGCCCCCGGCTCCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 616
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Db 617 TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 676
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Db 797 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 856
Qy 301 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360

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QY      421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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Db      977 TGCGCAACCCGGCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 1036
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QY      541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 600
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QY      601 AACTCAGGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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QY      721 ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
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Db      1337 TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGT 1396
QY      841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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RESULT 9

AR098146

LOCUS AR098146 1476 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 7 from patent US 6074841.

ACCESSION AR098146

VERSION AR098146.1 GI:12807403

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1476)

AUTHORS Gearing, D.P. and Busfield, S.J.

TITLE Don-1 gene and polypeptides and uses therefor

JOURNAL Patent: US 6074841-A 7 13-JUN-2000;

FEATURES Location/Qualifiers

source 1. .1476

/organism="unknown"

BASE COUNT 335 a 473 c 452 g 216 t
ORIGIN

Query Match 47.7%; Score 427.8; DB 6; Length 1476;
Best Local Similarity 89.8%; Pred. No. 1.4e-71;
Matches 459; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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QY      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
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Db      158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

QY      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
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Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

QY      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 602
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Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 337

QY      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
          |||||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

QY      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
          |||||
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

QY      723 CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
          |||||
Db      458 CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517

QY      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
          |||||
Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAATGTCC 577

QY      843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
          |||| | || | || || | ||
Db      578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608
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RESULT 10

AR116618

LOCUS AR116618 1476 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 7 from patent US 6133423.

ACCESSION AR116618

VERSION AR116618.1 GI:14096940

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1476)

AUTHORS Gearing,D.P. and Busfield,S.J.

TITLE Don-1 gene and polypeptides and uses therefor

JOURNAL Patent: US 6133423-A 7 17-OCT-2000;
FEATURES Location/Qualifiers
source 1. .1476
/organism="unknown"
BASE COUNT 335 a 473 c 452 g 216 t
ORIGIN

Query Match 47.7%; Score 427.8; DB 6; Length 1476;
Best Local Similarity 89.8%; Pred. No. 1.4e-71;
Matches 459; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Qy 363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
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Db 98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy 423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
    |||||||||||||||||||||||||||||||||||||||
Db 158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy 483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
    |||||||||||||||||||||||||||||||||||||||
Db 218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy 543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 602
    |||||||||||||||||||||||||||||||||||||||
Db 278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy 603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
    |||||||||||||||||||||||||||||||||||||||
Db 338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy 663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
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Db 398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

Qy 723 CACCCTGTCATCCTGGTCTGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
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Db 458 CACCCTGTCATCCTGGTCTGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517

Qy 783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
    |||||||||||||||||||||||||||||||||||||||
Db 518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577

Qy 843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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Db 578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608
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RESULT 11

AR098155

LOCUS AR098155 2268 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 31 from patent US 6074841.
ACCESSION AR098155
VERSION AR098155.1 GI:12807412
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
 REFERENCE 1 (bases 1 to 2268)
 AUTHORS Gearing, D.P. and Busfield, S.J.
 TITLE Don-1 gene and polypeptides and uses therefor
 JOURNAL Patent: US 6074841-A 31 13-JUN-2000;
 FEATURES Location/Qualifiers
 source 1. .2268
 /organism="unknown"
 BASE COUNT 502 a 734 c 701 g 331 t
 ORIGIN

Query Match 47.7%; Score 427.8; DB 6; Length 2268;
 Best Local Similarity 89.8%; Pred. No. 1.4e-71;
 Matches 459; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
          || || | || | | | | | | | | | | | | | | | |
Db      98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
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Db      158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
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Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 602
          |||||
Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
          |||||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
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Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

Qy      723 CACCCTGTTCATCCTGGTCGGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
          |||||
Db      458 CACCCTGTTCATCCTGGTCGGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517

Qy      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
          |||||
Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577

Qy      843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
          |||| | || | || | || |
Db      578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608
  
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RESULT 12
 AR116627
 LOCUS AR116627 2268 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 31 from patent US 6133423.
 ACCESSION AR116627

VERSION AR116627.1 GI:14096949
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 2268)
 AUTHORS Gearing, D.P. and Busfield, S.J.
 TITLE Don-1 gene and polypeptides and uses therefor
 JOURNAL Patent: US 6133423-A 31 17-OCT-2000;
 FEATURES Location/Qualifiers
 source 1. .2268
 /organism="unknown"
 BASE COUNT 502 a 734 c 701 g 331 t
 ORIGIN

Query Match 47.7%; Score 427.8; DB 6; Length 2268;
 Best Local Similarity 89.8%; Pred. No. 1.4e-71;
 Matches 459; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
      || || | || | || | || | || | || | || | || |
Db      98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
      |||||
Db      158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
      |||||
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 602
      |||||
Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
      |||||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
      |||||
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

Qy      723 CACCCTGTTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
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Db      458 CACCCTGTTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517

Qy      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAAGTGTCC 842
      |||||
Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577

Qy      843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
      |||| | || | || | || | || |
Db      578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608
  
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RESULT 13

AB001576
 LOCUS AB001576 2188 bp mRNA linear ROD 13-FEB-1999
 DEFINITION Rattus sp. mRNA for NTAK alpha2-1p, partial cds.
 ACCESSION AB001576
 VERSION AB001576.1 GI:2605478
 KEYWORDS neural- and thymus-derived activator for ErbB kinases.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (sites)
 AUTHORS Higashiyama, S., Horikawa, M., Yamada, K., Ichino, N., Nakano, N.,
 Nakagawa, T., Miyagawa, J., Matsushita, N., Nagatsu, T., Taniguchi, N.
 and Ishiguro, H.
 TITLE A novel brain-derived member of the epidermal growth factor family
 that interacts with ErbB3 and ErbB4
 JOURNAL J. Biochem. 122 (3), 675-680 (1997)
 MEDLINE 98006324
 PUBMED 9348101
 REFERENCE 2 (bases 1 to 2188)
 AUTHORS Ishiguro, H.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAR-1997) Hiroshi Ishiguro, Fujita Health University,
 ICMS; 1-98, kutsukake-cho, Toyoake, Aichi 470-11, Japan
 (E-mail:hishi@fujita-hu.ac.jp, Tel:0562-93-9393, Fax:0562-93-8831)
 FEATURES
 source Location/Qualifiers
 1. .2188
 /organism="Rattus sp."
 /mol_type="mRNA"
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 /cell_line="PC12"
 /cell_type="pheochromocytoma"
 CDS
 <1. .1926
 /note="neural- and thymus-derived activator for ErbB
 kinases (NTAK); a member of the epidermal growth factor
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 /product="NTAK alpha2-1p"
 /protein_id="BAA23348.1"
 /db_xref="GI:2605479"
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 AGEYVCEAENILGKDTVGRHLVNSVSTTLSSWSGHARKCNETAKSYCVNGGVCYYIE
 GINQLSCKCPNGFFGQRCLEKLPLRLYMPDPKQKAEELYQKRVLTITGICVALLVVGI
 VCVVAYCKTKKQRRQMHHHLRQNMCPAHQNRSLANGPSHPRLDPEEIQMADYISKVNP
 ATDHVIRREAETTFSGSHSCSPSHHCSTATPTSSHRHESHTWSLERSSELTSDSQSGI
 MLSSVGTSKCN SPACVEARARRAAAYSQEERRRAAMPPYHDSIDSLRDS PHSERVSA
 LTPARLSPVDFHYSLATQVPTFEITSPNSAHAVSLPPAAPISYRLAEQQPLLRHPAP
 PGP GPGADMQRSYDSYYP AAGPGPRRGACALGGS LGS LPASPFRI PEDDEYETQ
 ECAPPPPPRPRTRGASRRTSAGPRRWRRSRLNGLAAQRARAARDLSLSGSGCGSAS
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 RHSRGPPTRAKQDSGPL"
 BASE COUNT 515 a 674 c 643 g 356 t
 ORIGIN
 Query Match 47.4%; Score 425; DB 10; Length 2188;

Best Local Similarity 87.0%; Pred. No. 4.7e-71;
Matches 467; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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QY      337 TTAGTCTTTAAGACGGCCTTTGCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAG 396
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Db      4 TTTT TTTT TTAAGACAGCCTTTGCCCCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAG 63

QY      397 GTGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGC 456
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      64 GTGGGCAAGATCCTGTGCACTGACTGCGCAACCCGGCCCAAGCTGAAGAAGATGAAGAGT 123

QY      457 CAGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCC 516
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Db      124 CAGACAGGAGAGGTGGGCGAGAAGCAGTCGCTCAAGTGTGAGGCGGCGGGGGAACCCC 183

QY      517 CAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGC 576
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      184 CAGCCCTCCTATCGATGGTTCAAGGACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGC 243

QY      577 ATCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAG 636
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Db      244 ATCAAGTATGGCAACGGCAGAAAGAACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAG 303

QY      637 GACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGC 696
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Db      304 GACGCTGGAGAGTACGTCTGTGAGGCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGC 363

QY      697 CGGCTTTACGTCAACAGCGTGAGCACCACCTGTGCATCCTGGTCCGGGGCACGCCCCGGAAG 756
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Db      364 CGGCTCCATGTCAACAGTGTGAGCACCCTGTGTCGTCCTGGTCCGGGGCACGCCCCGGAAG 423

QY      757 TGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGC 816
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Db      424 TGCAATGAGACAGCCAAGTCCTACTGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGC 483

QY      817 ATCAACCAGCTCTCCTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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Db      484 ATCAACCAACTCTCCTGCAAATGTCCAAACGGATTCTTCGGACAGAGATGTTTGGAG 540

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RESULT 14

AC094080

LOCUS

AC094080

118504 bp

DNA

linear

PRI 27-MAR-2002

DEFINITION

Homo sapiens chromosome 5 clone CTB-77K22, complete sequence.

ACCESSION

AC094080

VERSION

AC094080.4 GI:19747152

KEYWORDS

HTG.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 118504)

AUTHORS

DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE

Direct Submission

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 118504)

AUTHORS

DOE Joint Genome Institute.

TITLE Direct Submission
 JOURNAL Submitted (14-SEP-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 3 (bases 1 to 118504)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 4 (bases 1 to 118504)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (27-MAR-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT On Mar 27, 2002 this sequence version replaced gi:19224838.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www-shgc.stanford.edu
 Quality: Phrap Quality >=40 99.7% of Sequence;
 Estimated Total Number of Errors is 0.5.
 FEATURES Location/Qualifiers
 source 1. .118504
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="CTB-77K22"
 BASE COUNT 33986 a 23829 c 24682 g 36007 t
 ORIGIN

Query Match 47.4%; Score 424.8; DB 9; Length 118504;
 Best Local Similarity 94.2%; Pred. No. 3.9e-71;
 Matches 452; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

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 Db 80890 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 80949
 QY 61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
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 Db 80950 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 81009
 QY 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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 Db 81010 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 81069
 QY 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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 Db 81070 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 81129
 QY 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
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 Db 81130 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 81189
 QY 301 CGCTACATCTTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
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 Db 81190 CGCTACATCTTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 81249

Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	81250	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	81309
Qy	421	TGC-GCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAA	479
Db	81310	TGCGGTGAGTCGCCCCCTCCCTTTGCTGGAGAAAGGGGGGAGGGGCGAGGTGGTGGAGAA	81369

RESULT 15
AC011589/c

LOCUS AC011589 152838 bp DNA linear HTG 30-MAR-2000
DEFINITION Homo sapiens clone RP11-13O18, WORKING DRAFT SEQUENCE, 10 unordered
pieces.

ACCESSION AC011589

VERSION AC011589.3 GI:7341917

KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 152838)

AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

TITLE Homo sapiens, clone RP11-13018

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 152838)

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

TITLE Direct Submission

JOURNAL Submitted (07-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On Mar 30, 2000 this sequence version replaced qi:6139107.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L3375

Center clone name: 13 0 18

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 147077 bases at least Q40
 Consensus quality: 149570 bases at least Q30
 Consensus quality: 150764 bases at least Q20
 Insert size: 188000; agarose-fp
 Insert size: 151938; sum-of-contigs
 Quality coverage: 4.4 in Q20 bases; agarose-fp
 Quality coverage: 5.4 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1840: contig of 1840 bp in length
 * 1841 1940: gap of 100 bp
 * 1941 5083: contig of 3143 bp in length
 * 5084 5183: gap of 100 bp
 * 5184 6473: contig of 1290 bp in length
 * 6474 6573: gap of 100 bp
 * 6574 11402: contig of 4829 bp in length
 * 11403 11502: gap of 100 bp
 * 11503 25453: contig of 13951 bp in length
 * 25454 25553: gap of 100 bp
 * 25554 40778: contig of 15225 bp in length
 * 40779 40878: gap of 100 bp
 * 40879 58024: contig of 17146 bp in length
 * 58025 58124: gap of 100 bp
 * 58125 87982: contig of 29858 bp in length
 * 87983 88082: gap of 100 bp
 * 88083 121177: contig of 33095 bp in length
 * 121178 121277: gap of 100 bp
 * 121278 152838: contig of 31561 bp in length.

FEATURES	Location/Qualifiers
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misc_feature	1941. .5083 /note="assembly_fragment"
misc_feature	5184. .6473 /note="assembly_fragment" clone_end:SP6 vector_side:right"
misc_feature	6574. .11402 /note="assembly_fragment"
misc_feature	11503. .25453 /note="assembly_fragment"

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                  /note="assembly_fragment"
misc_feature      40879. .58024
                  /note="assembly_fragment"
misc_feature      58125. .87982
                  /note="assembly_fragment"
misc_feature      88083. .121177
                  /note="assembly_fragment"
misc_feature      121278. .152838
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BASE COUNT 43896 a 33588 c 32260 g 42194 t 900 others
ORIGIN

Query Match 47.4%; Score 424.8; DB 2; Length 152838;
Best Local Similarity 94.2%; Pred. No. 3.8e-71;
Matches 452; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC 60
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Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
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Qy      181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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Db      54136 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 54077

Qy      301 CGCTACATCTTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
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Qy      421 TGC-GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAA 479
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Search completed: January 14, 2004, 10:22:59
Job time : 3591.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 07:12:21 ; Search time 290.304 Seconds
(without alignments)
8340.911 Million cell updates/sec

Title: US-09-864-675-3
Perfect score: 897
Sequence: 1 atgaggcgcgacccggcccc.....caatgggtcaacttctcctaa 897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	897	100.0	897	24	AAS18020	Human cDNA encodin	
2	849	94.6	994	24	AAS18019	Human cDNA encodin	
3	835.4	93.1	1884	19	AAV17814	Homo sapiens don-1	
4	784	87.4	3441	18	AAT87922	Rat cerebellum der	
5	738.6	82.3	1803	18	AAT87923	Rat cerebellum der	
6	737	82.2	3076	19	AAV43674	Receptor type tyro	
7	723.4	80.6	1863	25	ABS56035	cDNA encoding huma	
8	427.8	47.7	2268	19	AAV17816	Homo sapiens don-1	
9	426.8	47.6	1474	25	ABS56036	cDNA encoding huma	
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11	426.2	47.5	1476	19	AAV17815	Homo sapiens don-1	
12	424	47.3	1054	24	ABL40993	Human neuregulin 2	
13	405.4	45.2	1607	19	AAV17813	Mus musculus don-1	
14	402.2	44.8	2467	19	AAV17812	Mus musculus don-1	
15	393.4	43.9	1561	25	ABS56034	cDNA encoding muri	
16	393.4	43.9	2442	25	ABS56033	cDNA encoding muri	
17	256	28.5	667	18	AAT87924	Human cerebellum d	
18	173	19.3	419	24	ABL40994	Human neuregulin 2	
19	124.6	13.9	480	24	ABL40995	Human neuregulin 2	
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21	85.6	9.5	1986	20	AAZ32061	Human METH2 relate	
22	84	9.4	1986	22	AAC90318	L12260 cDNA clone.	
23	84	9.4	2003	17	AAT48090	Human neuregulin G	
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25	84	9.4	2003	17	AAT06739	Glial growth facto	
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27	84	9.4	2003	22	AAC90319	I36352 cDNA clone.	
28	83.4	9.3	1108	13	AAQ30671	GGF2BPP3.CDS. Syn	
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31	83.4	9.3	1108	16	AAQ74886	Putative bovine gl	
32	83.4	9.3	1108	17	AAT48080	Bovine neuregulin	
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35	82.4	9.2	2003	15	AAQ62838	GGF2HBS5. Homo sa	
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43	76.8	8.6	1140	17	AAT31001	Glial growth facto	
44	76.8	8.6	1140	17	AAT06731	BPP2 glial growth	
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ALIGNMENTS

RESULT 1

AAS18020

ID AAS18020 standard; cDNA; 897 BP.

XX

AC AAS18020;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human cDNA encoding Neuregulin-2beta, NRG-2beta.

XX

KW Human; ss; neuregulin-2; NRG-2alpha; NRG-2beta; mitogenesis;
 KW cell survival; cell growth; cell differentiation; erbB receptor;
 KW cardiomyopathy; ischaemic damage; cardiac trauma; heart failure;
 KW atherosclerosis; vascular lesion; vascular hypertension;
 KW degenerative congenital vascular disease; myasthenia gravis;
 KW neurodegenerative disorder; peripheral neuropathy;
 KW sensory nerve fiber neuropathy; motor fiber neuropathy;
 KW sensory nerve fiber neuropathy; multiple sclerosis;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve injury;
 KW Alzheimer's disease; Parkinson's disease; cerebellar ataxia;
 KW spinal cord injury; tumour; neurofibromatosis; transgenic animal.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	1..897
FT		/*tag= a
FT		/product= "NRG-2beta"

XX

PN WO200189568-A1.

XX

PD 29-NOV-2001.

XX

PF 23-MAY-2001; 2001WO-US16896.

XX

PR 23-MAY-2000; 2000US-206495P.

XX

PA (CENE-) CENES PHARM INC.

XX

PI Marchionni MA;

XX

DR WPI; 2002-097612/13.

DR

P-PSDB; AAU11636.

XX

PT Neuregulin-2 polypeptide and polynucleotide useful for treating
 PT multiple sclerosis, spinal muscular atrophy, nerve injury, Alzheimer's
 PT disease, by increasing mitogenesis, survival, growth or differentiation
 PT of a cell -

XX

PS Claim 57; Fig 8; 79pp; English.

XX

CC The invention relates to a substantially pure neuregulin (NRG)-2
 CC polypeptide comprising or consisting of a sequence for human
 CC NRG-2alpha or NRG-2beta (clone 2b7) and the polynucleotides encoding
 CC the. Also included are a vector expressing the protein, a host cell
 CC comprising the vector, a transgenic non-human animal transformed with

CC the vector or having a knockout mutation in one or both NRG-2
 CC alleles and an anti-NRG-2 antibody. Analysis of mutations in NRG-2 in an
 CC individual is useful for diagnosing an increased likelihood of
 CC developing a NRG-2-related disease or condition in a test subject.
 CC NRG-2 is useful for increasing the mitogenesis, survival, growth or
 CC differentiation of a cell (e.g. a neuronal cell), where the cell
 CC expresses an erbB receptor. NRG-2 is useful for treating diseases
 CC and disorders such as cardiomyopathy (preferably degenerative congenital
 CC disease), ischaemic damage, cardiac trauma or heart failure or which
 CC has a condition affecting smooth muscle which include atherosclerosis,
 CC vascular lesion, vascular hypertension, and degenerative congenital
 CC vascular disease, myasthenia gravis, a neurodegenerative disorder,
 CC peripheral neuropathy, a sensory nerve fiber neuropathy, a motor fiber
 CC and a sensory nerve fiber neuropathy, multiple sclerosis, amyotrophic
 CC lateral sclerosis, spinal muscular atrophy, nerve injury, Alzheimer's
 CC disease, Parkinson's disease, cerebellar ataxia, and spinal cord injury.
 CC The antibody is useful for treatment of a tumour comprising inhibiting
 CC proliferation of a tumour cell preferably a glial tumour cell, for
 CC treating of neurofibromatosis by inhibiting glial cell mitogenesis.
 CC The present sequence encodes NRG-2beta.

XX

SQ Sequence 897 BP; 200 A; 261 C; 282 G; 154 T; 0 other;

Query Match 100.0%; Score 897; DB 24; Length 897;
 Best Local Similarity 100.0%; Pred. No. 2.4e-199;
 Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC	60
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Qy	61	TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	61	TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
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Db	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Qy	301	CGCTACATCTTTTCTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	301	CGCTACATCTTTTCTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Qy	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480

Db	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
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Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
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Db	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Qy	721	ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	721	ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Db	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Qy	841	CCTGTGGGATACACCGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTCCTAA	897
Db	841	CCTGTGGGATACACCGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTCCTAA	897

RESULT 2

AAS18019

ID AAS18019 standard; cDNA; 994 BP.

XX

AC AAS18019;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human cDNA encoding Neuregulin-2alpha, NRG-2alpha.

XX

KW Human; ss; neuregulin-2; NRG-2alpha; NRG-2beta; mitogenesis;
 KW cell survival; cell growth; cell differentiation; erbB receptor;
 KW cardiomyopathy; ischaemic damage; cardiac trauma; heart failure;
 KW atherosclerosis; vascular lesion; vascular hypertension;
 KW degenerative congenital vascular disease; myasthenia gravis;
 KW neurodegenerative disorder; peripheral neuropathy;
 KW sensory nerve fiber neuropathy; motor fiber neuropathy;
 KW sensory nerve fiber neuropathy; multiple sclerosis;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve injury;
 KW Alzheimer's disease; Parkinson's disease; cerebellar ataxia;
 KW spinal cord injury; tumour; neurofibromatosis; transgenic animal.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..993

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FT          /*tag= a
FT          /product= "NRG-2alpha"
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PN  WO200189568-A1.
XX
PD  29-NOV-2001.
XX
PF  23-MAY-2001; 2001WO-US16896.
XX
PR  23-MAY-2000; 2000US-206495P.
XX
PA  (CENE-) CENES PHARM INC.
XX
PI  Marchionni MA;
XX
DR  WPI; 2002-097612/13.
DR  P-PSDB; AAU11635.
XX
PT  Neuregulin-2 polypeptide and polynucleotide useful for treating
PT  multiple sclerosis, spinal muscular atrophy, nerve injury, Alzheimer's
PT  disease, by increasing mitogenesis, survival, growth or differentiation
PT  of a cell -
XX
PS  Claim 57; Fig 6; 79pp; English.
XX
CC  The invention relates to a substantially pure neuregulin (NRG)-2
CC  polypeptide comprising or consisting of a sequence for human
CC  NRG-2alpha or NRG-2beta (clone 2b7) and the polynucleotides encoding
CC  the. Also included are a vector expressing the protein, a host cell
CC  comprising the vector, a transgenic non-human animal transformed with
CC  the vector or having a knockout mutation in one or both NRG-2
CC  alleles and an anti-NRG-2 antibody. Analysis of mutations in NRG-2 in an
CC  individual is useful for diagnosing an increased likelihood of
CC  developing a NRG-2-related disease or condition in a test subject.
CC  NRG-2 is useful for increasing the mitogenesis, survival, growth or
CC  differentiation of a cell (e.g. a neuronal cell), where the cell
CC  expresses an erbB receptor. NRG-2 is useful for treating diseases
CC  and disorders such as cardiomyopathy (preferably degenerative congenital
CC  disease), ischaemic damage, cardiac trauma or heart failure or which
CC  has a condition affecting smooth muscle which include atherosclerosis,
CC  vascular lesion, vascular hypertension, and degenerative congenital
CC  vascular disease, myasthenia gravis, a neurodegenerative disorder,
CC  peripheral neuropathy, a sensory nerve fiber neuropathy, a motor fiber
CC  and a sensory nerve fiber neuropathy, multiple sclerosis, amyotrophic
CC  lateral sclerosis, spinal muscular atrophy, nerve injury, Alzheimer's
CC  disease, Parkinson's disease, cerebellar ataxia, and spinal cord injury.
CC  The antibody is useful for treatment of a tumour comprising inhibiting
CC  proliferation of a tumour cell preferably a glial tumour cell, for
CC  treating of neurofibromatosis by inhibiting glial cell mitogenesis.
CC  The present sequence encodes NRG-2alpha.
XX
SQ  Sequence 994 BP; 230 A; 279 C; 304 G; 181 T; 0 other;

Query Match          94.6%; Score 849; DB 24; Length 994;
Best Local Similarity 98.3%; Pred. No. 3.6e-188;
Matches 858; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy	61	TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
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Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
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Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
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Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Qy	301	CGCTACATCTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	301	CGCTACATCTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
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Qy	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
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Db	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Qy	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Qy	721	ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	721	ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Db	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Qy	841	CCTGTGGGATACACCGGGGACAGGTGTCAGCAG	873

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RESULT 3

AAV17814

ID AAV17814 standard; cDNA; 1884 BP.

XX

AC AAV17814;

XX

DT 17-AUG-1998 (first entry)

XX

DE Homo sapiens don-1 gene splice variant.

XX

KW Murine; don-1 gene; melanoma; treatment; adenocarcinoma;

KW epithelial cell; proliferation; stimulation; treatment; tumours;

KW skin; oesophagus; lung; breast; liver; pancreas; colon; prostate;

KW gastrointestinal tract; uterus; wound healing; transmembrane; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 664..1884

FT /*tag= a

FT /note= "don-1 polypeptide"

XX

PN WO9807736-A1.

XX

PD 26-FEB-1998.

XX

PF 18-AUG-1997; 97WO-US14585.

XX

PR 19-NOV-1996; 96US-0753007.

PR 19-AUG-1996; 96US-0699591.

XX

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX

PI Busfield SJ, Gearing DP;

XX

DR WPI; 1998-169084/15.

DR P-PSDB; AAW48381.

XX

PT Mouse and human don-1 polypeptide(s) - useful for treatment of

PT melanomas and adenocarcinoma(s), and for wound healing

XX

PS Claim 4; Fig 3; 121pp; English.

XX

CC The sequence is that of a human don-1 gene splice variant.

CC Don-1 polypeptides stimulate proliferation of epithelial cells

CC and thus are implicated in melanomas and adenocarcinomas in which

CC epithelial cells proliferate out of control. Compounds that

CC interfere with don-1 mediated cell proliferation can be used

CC in the treatment of tumours such as melanomas and adenocarcinomas

CC of the skin, oesophagus, lung, breast, liver, pancreas,

CC gastrointestinal tract, colon, prostate or uterus. Alternatively,

CC don-1 polypeptides can be used to stimulate epithelial cell

CC proliferation, e.g. for wound healing.

XX

SQ Sequence 1884 BP; 426 A; 607 C; 560 G; 291 T; 0 other;

Query Match 93.1%; Score 835.4; DB 19; Length 1884;
Best Local Similarity 98.1%; Pred. No. 6.2e-185;
Matches 856; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

```
Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC 60
      |||
Db    218 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC 277

Qy     61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
      |||
Db    278 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 337

Qy    121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
      |||
Db    338 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 397

Qy    181 CCCGCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
      |||
Db    398 CCCGCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 457

Qy    241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
      |||
Db    458 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 517

Qy    301 CGCTACATCTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
      |||
Db    518 CGCTACATCTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 577

Qy    361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
      |||
Db    578 CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC 636

Qy    421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
      |||
Db    637 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 696

Qy    481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
      |||
Db    697 CAATCGCTGAAGTGTGAGGCAGCAGCCGGAATCCCCAGCCTTCCTACCGTTGGTTCAAG 756

Qy    541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG 600
      |||
Db    757 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG 816

Qy    601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
      |||
Db    817 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 876

Qy    661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
      |||
Db    877 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 936

Qy    721 ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
      |||
```

Db 937 ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 996
 QY 781 TGGCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
 |||||
 Db 997 TGGCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 1056
 QY 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
 || |||| | || | || || ||
 Db 1057 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 1089

RESULT 4

AAT87922

ID AAT87922 standard; cDNA; 3441 BP.

XX

AC AAT87922;

XX

DT 18-DEC-1997 (first entry)

XX

DE Rat cerebellum derived growth factor 1 cDNA.

XX

KW Rat; cerebellum derived growth factor; CDGF1; screening; binding;
 KW modulation; erbB type receptor; identification; indication; risk;
 KW proliferation; differentiation; induction; neuron; hyperplasia;
 KW stem cell culture; intracerebral graft; alleviation; repair;
 KW behavioural defect; nervous system; central; peripheral; nerve;
 KW prosthesis; damage; entubulation; cell survival; treatment;
 KW injury; trauma; ischaemia; ischemia; stroke; infection; disorder;
 KW inflammation; neurodegeneration; disease; Parkinson's;
 KW Huntingdon's; amyotrophic lateral sclerosis; sensory; retina;
 KW spinocerebellar degeneration; multiple sclerosis; neoplasia;
 KW amalignant glioma; medulloblastoma; neuroectodermal tumour; ds.

XX

OS Rattus rattus.

XX

FH Key Location/Qualifiers

FT CDS 180..2444

FT /*tag= a

FT sig_peptide 180..248

FT /*tag= b

FT mat_peptide 249..2441

FT /*tag= c

FT /product= cerebellum_derived_growth_factor

XX

PN W09709425-A1.

XX

PD 13-MAR-1997.

XX

PF 09-SEP-1996; 96WO-US14484.

XX

PR 08-SEP-1995; 95US-0525864.

XX

PA (HARD) HARVARD COLLEGE.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PA (STRD) UNIV LELAND S STANFORD.

XX

PI Chang H;

XX
 DR WPI; 1997-192900/17.
 DR P-PSDB; AAW27536.
 XX
 PT Rat and human cerebellum-derived growth factors - used in the
 PT treatment of neuronal injury and proliferative disorders
 XX
 PS Claim 17; Pages 63-66; 94pp; English.
 XX
 CC The present sequence encodes rat cerebellum derived growth factor 1
 CC (CDGF1), which can be used to screen for modulators of CDGF
 CC binding to erbB type receptors. Identification of a modification or
 CC mutation in a CDGF gene, or aberrant expression of a CDGF gene or
 CC levels of soluble CDGF may be used to indicate the risk of unwanted
 CC cell proliferation or differentiation.
 CC CDGF may be used to induce neuronal differentiation in stem cell
 CC culture, and maintain the integrity of a terminally differentiated
 CC neuronal cell culture, e.g. useful for intracerebral grafting to
 CC alleviate behavioural defects. CDGF may also be used in nerve
 CC protheses to repair central and peripheral nerve damage, especially
 CC where a crushed or severed axon is entubulated by a prosthetic.
 CC CDGF may also be used to enhance neuronal cell survival in the
 CC central or peripheral nervous system, to treat neurological
 CC conditions associated with nervous system injury, e.g. traumatic,
 CC chemical or vasal injury and deficits such as ischaemia resulting
 CC from stroke, infectious/inflammatory and tumour induced injury,
 CC chronic neurodegenerative disease including Parkinson's and
 CC Huntingdon's, amyotrophic lateral sclerosis, spinocerebellar
 CC degeneration, chronic immunological disease of the nervous system
 CC including multiple sclerosis, disorders of the sensory neurons and
 CC degenerative diseases of the retina. CDGF may also be used to treat
 CC neoplastic or hyperplastic transformations, particularly of the
 CC central nervous system, e.g. amalignant gliomas, medulloblastomas
 CC and neuroectodermal tumours.
 XX
 SQ Sequence 3441 BP; 777 A; 1057 C; 1015 G; 592 T; 0 other;

Query Match 87.4%; Score 784; DB 18; Length 3441;
 Best Local Similarity 92.2%; Pred. No. 6.7e-173;
 Matches 826; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCTCGCTCGCCTGC	60
Db	180	ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC	239
Qy	61	TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	240	TACTCGCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	299
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	300	GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT	359
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	360	CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	419

Qy 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
 |||
 Db 420 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 479
 Qy 301 CGCTACATCTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
 |||
 Db 480 CGCTACATCTTTTCTGGAGCCACCGAGCAGCCCTTAGTCTTTAAGACAGCCTTTGCC 539
 Qy 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
 || |||
 Db 540 CCGGTGCACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 599
 Qy 421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
 |||
 Db 600 TGCGCAACCCGGCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 659
 Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
 || |||
 Db 660 CAGTCGCTCAAGTGTGAGGCAGCGCGGGGAACCCCCAGCCCTCCTATCGATGGTTCAAG 719
 Qy 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 600
 || |||
 Db 720 GACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGCATCAAGTATGGCAACGGCAGAAAG 779
 Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
 |||
 Db 780 AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG 839
 Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
 || |||
 Db 840 GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC 899
 Qy 721 ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
 |||
 Db 900 ACCACTCTGTCGTCTGTTGGTTCGGGGCACGCCCCGGAAGTGCAATGAGACAGCCAAGTCCTAC 959
 Qy 781 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
 || |||
 Db 960 TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAGTGT 1019
 Qy 841 CCTGTGGGATACACCGGGACAGGTGTCAGCAGTTTCGCAATGGTCAACTTCTCCTA 896
 |||
 Db 1020 CCTGTGGGATACACCGGGACAGGTGTCAGCAGTTTCGCAATGGTCAACTTCTCCAA 1075

RESULT 5

AAT87923

ID AAT87923 standard; cDNA; 1803 BP.

XX

AC AAT87923;

XX

DT 18-DEC-1997 (first entry)

XX

DE Rat cerebellum derived growth factor 2 cDNA.

XX

KW Rat; cerebellum derived growth factor; CDGF2; screening; binding;

KW modulation; erbB type receptor; identification; indication; risk;

KW proliferation; differentiation; induction; neuron; hyperplasia;
 KW stem cell culture; intracerebral graft; alleviation; repair;
 KW behavioural defect; nervous system; central; peripheral; nerve;
 KW prosthesis; damage; entubulation; cell survival; treatment;
 KW injury; trauma; ischaemia; ischemia; stroke; infection; disorder;
 KW inflammation; neurodegeneration; disease; Parkinson's;
 KW Huntingdon's; amyotrophic lateral sclerosis; sensory; retina;
 KW spinocerebellar degeneration; multiple sclerosis; neoplasia;
 KW amalignant glioma; medulloblastoma; neuroectodermal tumour; ds.
 XX
 OS Rattus rattus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..993
 FT /*tag= a
 FT sig_peptide 1..69
 FT /*tag= b
 FT mat_peptide 70..990
 FT /*tag= c
 FT /product= cerebellum_derived_growth_factor
 XX
 PN WO9709425-A1.
 XX
 PD 13-MAR-1997.
 XX
 PF 09-SEP-1996; 96WO-US14484.
 XX
 PR 08-SEP-1995; 95US-0525864.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (STRD) UNIV LELAND S STANFORD.
 XX
 PI Chang H;
 XX
 DR WPI; 1997-192900/17.
 DR P-PSDB; AAW27537.
 XX
 PT Rat and human cerebellum-derived growth factors - used in the
 PT treatment of neuronal injury and proliferative disorders
 XX
 PS Claim 17; Pages 70-74; 94pp; English.
 XX
 CC The present sequence encodes rat cerebellum derived growth factor 2
 CC (CDGF2), which can be used to screen for modulators of CDGF
 CC binding to erbB type receptors. Identification of a modification or
 CC mutation in a CDGF gene, or aberrant expression of a CDGF gene or
 CC levels of soluble CDGF may be used to indicate the risk of unwanted
 CC cell proliferation or differentiation.
 CC CDGF may be used to induce neuronal differentiation in stem cell
 CC culture, and maintain the integrity of a terminally differentiated
 CC neuronal cell culture, e.g. useful for intracerebral grafting to
 CC alleviate behavioural defects. CDGF may also be used in nerve
 CC prostheses to repair central and peripheral nerve damage, especially
 CC where a crushed or severed axon is entubulated by a prosthetic.
 CC CDGF may also be used to enhance neuronal cell survival in the
 CC central or peripheral nervous system, to treat neurological

CC conditions associated with nervous system injury, e.g. traumatic,
 CC chemical or vasal injury and deficits such as ischaemia resulting
 CC from stroke, infectious/inflammatory and tumour induced injury,
 CC chronic neurodegenerative disease including Parkinson's and
 CC Huntingdon's, amyotrophic lateral sclerosis, spinocerebellar
 CC degeneration, chronic immunological disease of the nervous system
 CC including multiple sclerosis, disorders of the sensory neurons and
 CC degenerative diseases of the retina. CDGF may also be used to treat
 CC neoplastic or hyperplastic transformations, particularly of the
 CC central nervous system, e.g. amalignant gliomas, medulloblastomas
 CC and neuroectodermal tumours.

XX

SQ Sequence 1803 BP; 408 A; 549 C; 537 G; 309 T; 0 other;

Query Match 82.3%; Score 738.6; DB 18; Length 1803;
 Best Local Similarity 90.4%; Pred. No. 2.2e-162;
 Matches 789; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC	60
Db	1	ATGAGGCGCGACCCGGCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC	60
Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	61	TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	121	GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT	180
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	181	CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG	300
Qy	301	CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	301	CGCTACATCTTTTTCCTGGAGCCCACCGAGCAGCCCTTAGTCTTTAAGACAGCCTTTGCC	360
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	361	CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Qy	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	421	TGCGCAACCCGGCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG	480
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	481	CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCCAGCCCTCCTATCGATGGTTCAAG	540
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAAG	600
Db	541	GACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGCATCAAGTATGGCAACGGCAGAAAAG	600

[illegible]

XX

PS Examples; Pages 9-13; 17pp; Japanese.

XX

CC This cDNA encodes the ligand of receptor type tyrosine kinase ErbB. A
CC prokaryotic or eukaryotic host cell transformed by a recombinant vector
CC containing the encoding DNA can be used for the recombinant production of
CC the protein. The invention provides a method for inhibiting the formation
CC of the ligand of receptor type tyrosine kinase ErbB in an animal using
CC an antibody recognizing the protein. The ligand of the tyrosine kinase
CC ErbB receptor and associated materials can be used for treating or
CC diagnosing nervous diseases and cancers.

XX

SQ Sequence 3076 BP; 673 A; 996 C; 944 G; 463 T; 0 other;

Query Match 82.2%; Score 737; DB 19; Length 3076;

Best Local Similarity 90.3%; Pred. No. 5.8e-162;

Matches 788; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

```
QY      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCTCGCTCGCCTGC 60
      |||
DB      556 ATGAGGCGCGACCCGGCCCCCGGCTCCTCGATGCTGCTCTTCGGTGTGTCTACTCGCCTGC 615

QY      61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
      |||
DB      616 TACTCGCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 675

QY     121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
      |||
DB      676 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT 735

QY     181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
      |||
DB      736 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 795

QY     241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
      |||
DB      796 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 855

QY     301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
      |||
DB      856 CGCTACATCTTTTTCCTGGAGCCACCGAGCAGCCCTTAGTCTTTAAGACAGCCTTTGCC 915

QY     361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
      ||
DB      916 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 975

QY     421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
      |||
DB      976 TGCGCAACCCGGCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 1035

QY     481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
      ||
DB     1036 CAGTCGCTCAAGTGTGAGGCGGCGGCGGGGAACCCCCAGCCCTCCTATCGATGGTTCAAG 1095

QY     541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAAG 600
      ||
DB     1096 GACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGCATCAAGTATGGCAACGGCAGAAAAG 1155
```


XX
 PI Gearing DP, Busfield SJ;
 XX
 DR WPI; 2003-039584/03.
 DR P-PSDB; ABG71638.
 XX
 PT Novel Don-1 polypeptide useful for stimulating proliferation of cells,
 PT for identifying proteins that interact with Don-1, and for regulating
 PT tumour formation and progression in brain -
 XX
 PS Claim 4; Fig 3; 66pp; English.
 XX

CC The present invention relates to the isolation of a novel gene
 CC called Don-1, and alternate splice variants of Don-1, which are
 CC related to epidermal growth factors (EGF) such as neuregulins.
 CC Don-1 polypeptides are glycoprotein ligands. Both murine and human
 CC Don-1 sequences are cloned. The mouse Don-1 gene maps to chromosome 18.
 CC Don-1 polypeptides are useful for stimulating proliferation of a cell.
 CC Antibodies to Don-1 polypeptides are useful for detecting Don-1
 CC in a sample. The Don-1 polypeptides are useful for treating and
 CC diagnosing cell proliferative disorders and play a role in the
 CC proliferation of carcinomas e.g. adenocarcinoma, myeloma, in cell
 CC differentiation, proliferation and survival. The polypeptides are
 CC also useful for inhibiting proliferation of adenocarcinoma cells,
 CC for stimulating the proliferation of cells such as epithelial cells
 CC to promote wound healing, for identifying proteins that interact
 CC with Don-1, and for regulating tumour formation and progression in
 CC the brain. The polynucleotide sequences encoding Don-1 may be used
 CC in gene therapy. The present sequence encodes human membrane-bound
 CC splice variant of Don-1.
 XX

XX
 SQ Sequence 1863 BP; 422 A; 602 C; 553 G; 286 T; 0 other;

Query Match 80.6%; Score 723.4; DB 25; Length 1863;
 Best Local Similarity 96.2%; Pred. No. 7.5e-159;
 Matches 840; Conservative 0; Mismatches 16; Indels 17; Gaps 9;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC	60
Db	213	ATGAGGCGCGACCCGGCCCC--CTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC	270
Qy	61	TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	271	TACTCGCCAGCCTCAAGTCA--GCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	328
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	329	GGCAAGGTACAGGGGCTGGT--CAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	386
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGCCGCTCCGGAGCGGG	240
Db	387	CCCGCCTCGGGTCGGGTGGCG--GGTAAAGGTGCTGGACAAGTGCCGCTCCGGAGCGGG	444
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	445	GGGCTGCAGCGCGAGCAGGTG--CAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	502

Qy 301 CGCTACATCTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
 |||
 Db 503 CGCTACATCTTTTCTGGAG--CACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 560
 Qy 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
 |||
 Db 561 CCCCT-GATACCAACGGCAAAA--CTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC 617
 Qy 421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
 |||
 Db 618 TGCGCCACCCGGCCCAAGTTGA--AAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 675
 Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
 |||
 Db 676 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 735
 Qy 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 600
 |||
 Db 736 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 795
 Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
 |||
 Db 796 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 855
 Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
 |||
 Db 856 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 915
 Qy 721 ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
 |||
 Db 916 ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 975
 Qy 781 TGCCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
 |||
 Db 976 TGCCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 1035
 Qy 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
 ||
 Db 1036 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 1068

RESULT 8

AAV17816

ID AAV17816 standard; cDNA; 2268 BP.

XX

AC AAV17816;

XX

DT 17-AUG-1998 (first entry)

XX

DE Homo sapiens don-1 gene splice variant.

XX

KW Murine; don-1 gene; melanoma; treatment; adenocarcinoma;

KW epithelial cell; proliferation; stimulation; treatment; tumours;

KW skin; oesophagus; lung; breast; liver; pancreas; colon; prostate;

KW gastrointestinal tract; uterus; wound healing; transmembrane; ss.

XX

OS Homo sapiens.


```

XX
FH   Key                      Location/Qualifiers
FT   CDS                      69..2012
FT                                  /*tag=  a
FT                                  /note= "don-1 polypeptide"
XX
PN   WO9807736-A1.
XX
PD   26-FEB-1998.
XX
PF   18-AUG-1997;    97WO-US14585.
XX
PR   19-NOV-1996;    96US-0753007.
PR   19-AUG-1996;    96US-0699591.
XX
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI   Busfield SJ,  Gearing DP;
XX
DR   WPI; 1998-169084/15.
DR   P-PSDB; AAW48383.
XX
PT   Mouse and human don-1 polypeptide(s) - useful for treatment of
PT   melanomas and adenocarcinoma(s), and for wound healing
XX
PS   Claim 4; Fig 7; 121pp; English.
XX
CC   The sequence is that of a human don-1 gene splice variant.
CC   Don-1 polypeptides stimulate proliferation of epithelial cells
CC   and thus are implicated in melanomas and adenocarcinomas in which
CC   epithelial cells proliferate out of control. Compounds that
CC   interfere with don-1 mediated cell proliferation can be used
CC   in the treatment of tumours such as melanomas and adenocarcinomas
CC   of the skin, oesophagus, lung, breast, liver, pancreas,
CC   gastrointestinal tract, colon, prostate or uterus. Alternatively,
CC   don-1 polypeptides can be used to stimulate epithelial cell
CC   proliferation, e.g. for wound healing.
XX
SQ   Sequence 2268 BP; 502 A; 735 C; 700 G; 331 T; 0 other;

Query Match          47.7%;  Score 427.8;  DB 19;  Length 2268;
Best Local Similarity  89.8%;  Pred. No. 5.4e-90;
Matches 459;  Conservative  0;  Mismatches  52;  Indels  0;  Gaps  0;

Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
      || || | || | | | | | | | | | | | | | | | |
Db      98  CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
      |||||
Db      158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
      |||||
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 602

```

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Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 337
Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397
Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457
Qy      723 CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
Db      458 CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517
Qy      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577
Qy      843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
Db      578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608

```

RESULT 9

ABS56036

ID ABS56036 standard; cDNA; 1474 BP.

XX

AC ABS56036;

XX

DT 14-JAN-2003 (first entry)

XX

DE cDNA encoding human second splice variant of Don-1.

XX

KW Human; Don-1; epidermal growth factor; EGF; neuregulin;

KW glycoprotein ligand; cell proliferation; cell proliferative disorder;

KW carcinoma; adenocarcinoma cell; myeloma; cell differentiation;

KW cell survival; epithelial cell; wound healing; tumour formation;

KW brain; vulnerary; cytostatic; gene therapy; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 68..1473

FT /*tag= a

FT /partial

FT /product= "Second splice variant of Don-1"

FT /note= "This sequence lacks a stop codon"

FT /transl_except= (pos:107..108, aa:Lys)

FT /note= "This codon has an apparent 1 nucleotide
deletion which alters the reading frame"

XX

PN US2002127594-A1.

XX

PD 12-SEP-2002.

XX

PF 12-MAR-2002; 2002US-0096241.

XX
PR 22-JUN-2000; 2000US-0599789.

PA (GEAR/) GEARING D P.
PA (BUSF/) BUSFIELD S J.

PI Gearing DP, Busfield SJ;

XX
DR WPI; 2003-039584/03.

XX
PT Novel Don-1 polypeptide useful for stimulating proliferation of cells,
PT for identifying proteins that interact with Don-1, and for regulating
PT tumour formation and progression in brain -

PS Claim 4; Fig 4; 66pp; English.

XX
CC The present invention relates to the isolation of a novel gene
CC called Don-1, and alternate splice variants of Don-1, which are
CC related to epidermal growth factors (EGF) such as neuregulins.
CC Don-1 polypeptides are glycoprotein ligands. Both murine and human
CC Don-1 sequences are cloned. The mouse Don-1 gene maps to chromosome 18.
CC Don-1 polypeptides are useful for stimulating proliferation of a cell.
CC Antibodies to Don-1 polypeptides are useful for detecting Don-1
CC in a sample. The Don-1 polypeptides are useful for treating and
CC diagnosing cell proliferative disorders and play a role in the
CC proliferation of carcinomas e.g. adenocarcinoma, myeloma, in cell
CC differentiation, proliferation and survival. The polypeptides are
CC also useful for inhibiting proliferation of adenocarcinoma cells,
CC for stimulating the proliferation of cells such as epithelial cells
CC to promote wound healing, for identifying proteins that interact
CC with Don-1, and for regulating tumour formation and progression in
CC the brain. The polynucleotide sequences encoding Don-1 may be used
CC in gene therapy. The present sequence encodes human second
CC splice variant of Don-1.

SQ Sequence 1474 BP; 335 A; 472 C; 451 G; 216 T; 0 other;

Query Match 47.6%; Score 426.8; DB 25; Length 1474;
Best Local Similarity 92.4%; Pred. No. 8.3e-90;
Matches 449; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy	388	AAGAAAGAGGTTGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGCCCCAAGTTGAAGAAG	447
Db	121	AGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAAAGCCACCCGGCCCCAAGTTGAAGAAG	180
Qy	448	ATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCC	507
Db	181	ATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCC	240
Qy	508	GGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGA	567
Db	241	GGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGA	300
Qy	568	GACATTGCGCATCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTG	627
Db	301	GACATTGCGCATCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTG	360

QY 628 AAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACC 687
 |||
 Db 361 AAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACC 420
 QY 688 GTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGCAC 747
 |||
 Db 421 GTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGCAC 480
 QY 748 GCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTAC 807
 |||
 Db 481 GCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTAC 540
 QY 808 ATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGT 867
 |||
 Db 541 ATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGT 600
 QY 868 CAGCAG 873
 ||
 Db 601 TTGGAG 606

RESULT 10

ABS56045

ID ABS56045 standard; cDNA; 2266 BP.

XX

AC ABS56045;

XX

DT 14-JAN-2003 (first entry)

XX

DE cDNA encoding human third splice variant of Don-1.

XX

KW Human; Don-1; epidermal growth factor; EGF; neuregulin;

KW glycoprotein ligand; cell proliferation; cell proliferative disorder;

KW carcinoma; adenocarcinoma cell; myeloma; cell differentiation;

KW cell survival; epithelial cell; wound healing; tumour formation;

KW brain; vulnerary; cytostatic; gene therapy; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS

68..2010

FT /*tag= a

FT /product= "Third splice variant of Don-1"

FT /transl_except= (pos:107..108, aa:Lys)

FT /note= "This codon has an apparent 1 nucleotide
 deletion which alters the reading frame"

FT /transl_except= (pos:994..996, aa:Thr)

XX

PN US2002127594-A1.

XX

PD 12-SEP-2002.

XX

PF 12-MAR-2002; 2002US-0096241.

XX

PR 22-JUN-2000; 2000US-0599789.

XX

[illegible]

Db 361 AAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGGAAGGACACC 420
 QY 688 GTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGGCAC 747
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 GTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGGCAC 480
 QY 748 GCCCGBAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTAC 807
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 GCCCGBAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTAC 540
 QY 808 ATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGT 867
 |||||||||||||||||||||||||||||||||||||||| |||| | || | || ||
 Db 541 ATCGAGGGCATCAACCAGCTCTCCTGCAATGTCCAAATGGATTCTTCGGACAGAGATGT 600
 QY 868 CAGCAG 873
 | ||
 Db 601 TTGGAG 606

RESULT 11

AAV17815

ID AAV17815 standard; cDNA; 1476 BP.

XX

AC AAV17815;

XX

DT 17-AUG-1998 (first entry)

XX

DE Homo sapiens don-1 gene splice variant.

XX

KW Murine; don-1 gene; melanoma; treatment; adenocarcinoma;
 KW epithelial cell; proliferation; stimulation; treatment; tumours;
 KW skin; oesophagus; lung; breast; liver; pancreas; colon; prostate;
 KW gastrointestinal tract; uterus; wound healing; transmembrane; ss.
 XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	69..1475
FT		/*tag= a
FT		/note= "don-1 polypeptide"
XX		

PN W09807736-A1.

XX

PD 26-FEB-1998.

XX

PF 18-AUG-1997; 97WO-US14585.

XX

PR 19-NOV-1996; 96US-0753007.

PR 19-AUG-1996; 96US-0699591.

XX

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX

PI Busfield SJ, Gearing DP;

XX

DR WPI; 1998-169084/15.

DR P-PSDB; AAW48382.

XX

PT Mouse and human don-1 polypeptide(s) - useful for treatment of
PT melanomas and adenocarcinoma(s), and for wound healing

XX

PS Claim 4; Fig 4; 121pp; English.

XX

CC The sequence is that of a human don-1 gene splice variant.
CC Don-1 polypeptides stimulate proliferation of epithelial cells
CC and thus are implicated in melanomas and adenocarcinomas in which
CC epithelial cells proliferate out of control. Compounds that
CC interfere with don-1 mediated cell proliferation can be used
CC in the treatment of tumours such as melanomas and adenocarcinomas
CC of the skin, oesophagus, lung, breast, liver, pancreas,
CC gastrointestinal tract, colon, prostate or uterus. Alternatively,
CC don-1 polypeptides can be used to stimulate epithelial cell
CC proliferation, e.g. for wound healing.

XX

SQ Sequence 1476 BP; 335 A; 475 C; 450 G; 216 T; 0 other;

Query Match 47.5%; Score 426.2; DB 19; Length 1476;
Best Local Similarity 89.6%; Pred. No. 1.1e-89;
Matches 458; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY	363	CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG	422
Db	98	CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA	157
QY	423	CGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	482
Db	158	AGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	217
QY	483	ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	542
Db	218	ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	277
QY	543	TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA	602
Db	278	TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA	337
QY	603	CTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	662
Db	338	CTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	397
QY	663	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	722
Db	398	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	457
QY	723	CACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG	782
Db	458	CACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG	517
QY	783	CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC	842
Db	518	CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAATGTCC	577
QY	843	TGTGGGATACACCGGGGACAGGTGTCAGCAG	873
Db	578	AAATGGATTCTTCGCACAGAGATGTTTGGAG	608

RESULT 12

ABL40993

ID ABL40993 standard; DNA; 1054 BP.

XX

AC ABL40993;

XX

DT 03-JUL-2002 (first entry)

XX

DE Human neuregulin 2 gene exon 1.

XX

KW Human; MUC1; mucin; glycoprotein; cytostatic; cancer; tumour; ECD;
KW extracellular domain; neuregulin 2; isoform; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200222685-A2.

XX

PD 21-MAR-2002.

XX

PF 11-SEP-2001; 2001WO-US28548.

XX

PR 11-SEP-2000; 2000US-231841P.

XX

PA (KUFE/) KUFE D W.

PA (OHNO/) OHNO T.

XX

PI Kufe DW, Ohno T;

XX

DR WPI; 2002-339864/37.

XX

PT Use of a mucin glycoprotein (MUC1) extracellular domain antagonist for
PT manufacturing a medicant that inhibits the proliferation of MUC-1
PT expressing cancer cells and that can treat cancers and reduce tumor
PT growth -

XX

PS Disclosure; Page 61-62; 74pp; English.

XX

CC The invention relates to the use of a MUC1 (mucin glycoprotein)
CC extracellular domain (ECD) antagonist for the manufacture of a medicant
CC to inhibit the proliferation of MUC-1 expressing cancer cells. MUC1 ECD
CC antagonists (optionally combined with a pharmaceutical carrier) can be
CC administered to inhibit proliferation of MUC1-expressing cancer cells,
CC useful to treat cancers e.g. skin cancer, prostate cancer and leukemia,
CC especially in humans. The method may also be combined with administration
CC of a chemotherapeutic agent (e.g. an alkylating agent, topoisomerase etc)
CC or radiation to treat cancer, especially to reduce tumour growth. The
CC polypeptides are also useful in screening to identify MUC1 ECD
CC antagonists. The present sequence represents an exon fragment of the
CC human neuregulin 2 gene.

XX

SQ Sequence 1054 BP; 178 A; 367 C; 361 G; 148 T; 0 other;

Query Match 47.3%; Score 424; DB 24; Length 1054;

Best Local Similarity 100.0%; Pred. No. 3.4e-89;

Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
 |||
 Db 589 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 648
 QY 61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
 |||
 Db 649 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 708
 QY 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
 |||
 Db 709 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 768
 QY 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
 |||
 Db 769 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 828
 QY 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
 |||
 Db 829 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 888
 QY 301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
 |||
 Db 889 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 948
 QY 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
 |||
 Db 949 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 1008
 QY 421 TGCG 424
 |||
 Db 1009 TGCG 1012

RESULT 13

AAV17813

ID AAV17813 standard; cDNA; 1607 BP.

XX

AC AAV17813;

XX

DT 17-AUG-1998 (first entry)

XX

DE Mus musculus don-1 gene splice variant.

XX

KW Murine; don-1 gene; melanoma; treatment; adenocarcinoma;

KW epithelial cell; proliferation; stimulation; treatment; tumours;

KW skin; oesophagus; lung; breast; liver; pancreas; colon; prostate;

KW gastrointestinal tract; uterus; wound healing; secreted protein; ss.

XX

OS Mus musculus.

XX

FH Key

Location/Qualifiers

FT CDS

79..624

FT

/*tag= a

FT

/note= "secreted don-1 polypeptide"

XX

PN WO9807736-A1.

```
XX PD      26-FEB-1998.  
XX  
PF      18-AUG-1997;    97WO-US14585.  
XX  
PR      19-NOV-1996;    96US-0753007.  
PR      19-AUG-1996;    96US-0699591.  
XX  
PA      (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
XX  
PI      Busfield SJ,   Gearing DP;  
XX  
DR      WPI; 1998-169084/15.  
DR      P-PSDB; AAW48380.  
XX  
PT      Mouse and human don-1 polypeptide(s) - useful for treatment of  
PT      melanomas and adenocarcinoma(s), and for wound healing  
XX  
PS      Claim 4; Fig 2; 121pp; English.  
XX  
CC      The sequence is that of a murine don-1 gene splice variant.  
CC      Don-1 polypeptides stimulate proliferation of epithelial cells  
CC      and thus are implicated in melanomas and adenocarcinomas in which  
CC      epithelial cells proliferate out of control. Compounds that  
CC      interfere with don-1 mediated cell proliferation can be used  
CC      in the treatment of tumours such as melanomas and adenocarcinomas  
CC      of the skin, oesophagus, lung, breast, liver, pancreas,  
CC      gastrointestinal tract, colon, prostate or uterus. Alternatively,  
CC      don-1 polypeptides can be used to stimulate epithelial cell  
CC      proliferation, e.g. for wound healing.  
XX  
SQ      Sequence 1607 BP; 365 A; 500 C; 480 G; 262 T; 0 other;
```

Query Match 45.2%; Score 405.4; DB 19; Length 1607;
Best Local Similarity 87.9%; Pred. No. 8.2e-85;
Matches 442; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

```
QY      371 CCAACGGCAAATACTCAAGAAAGAGGTGGGCAAGATCCTGTGCGACTGACTGCCACCACCC 430  
        | |||||            |||||||  
Db       2 CTAAACGGCAAACAATCAAGAAAGAGGTGGGCAAGATCCTGTGCGACTGACTGCCACCACCC 61  
  
QY      431 GGCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGA 490  
        |||||            ||||||| || ||||||| |||||  
Db       62 GGCCAAGCTGAAGAAGATGAAGAGCCAGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCA 121  
  
QY      491 AGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGG 550  
        |||||            || || || ||||| |||| || |||||  
Db      122 AGTGTGAGGCAGCGCGGGAAACCCCAGCCCTCCTATCGCTGGTTCAGGATGGCAAGG 181  
  
QY      551 AGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGAC 610  
        | ||||| || || || ||||| ||||| || |||||  
Db     182 AACTCAACCGGAGTCGTGATATTTCGCATCAAGTATGGCAATGTCAGAAAGAACTCACGGC 241  
  
QY      611 TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA 670  
        |||||            |||| ||||| || ||||| |||||  
Db     242 TACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTACGTCTGTGAGGCCGAGAACA 301
```

QY 671 TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGT 730
 |||| |||||||||||||| |||||| || | |||||||||||||||||| ||||
 Db 302 TCCTTGGGAAGGACACCGTGAGGGGCGGACTCCATGTCAACAGCGTGAGCACCCTCTGT 361
 QY 731 CATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATG 790
 |||||||||||| || |||||||||||||| |||| |||||||||| || || ||||
 Db 362 CATCCTGGTCGGGACATGCCCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATG 421
 QY 791 GAGGCGTCTGCTACTACATCGAGGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGAT 850
 |||||| |||||||||||||||||||||||||||||||||| |||| ||||
 Db 422 GAGGCGTGTGCTACTACATCGAGGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGAT 481
 QY 851 ACACCGGGGACAGGTGTCAGCAG 873
 | ||| | || || | ||
 Db 482 TCTTCGGACAGAGATGTTTGGAG 504

RESULT 14

AAV17812

ID AAV17812 standard; cDNA; 2467 BP.

XX

AC AAV17812;

XX

DT 17-AUG-1998 (first entry)

XX

DE Mus musculus don-1 gene splice variant.

XX

KW Murine; don-1 gene; melanoma; treatment; adenocarcinoma;
 KW epithelial cell; proliferation; stimulation; treatment; tumours;
 KW skin; oesophagus; lung; breast; liver; pancreas; colon; prostate;
 KW gastrointestinal tract; uterus; wound healing; transmembrane; ss.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT CDS

79..1896

FT

/*tag= a

FT

/note= "transmembrane don-1 polypeptide"

XX

PN WO9807736-A1.

XX

PD 26-FEB-1998..

XX

PF 18-AUG-1997; 97WO-US14585.

XX

PR 19-NOV-1996; 96US-0753007.

PR

19-AUG-1996; 96US-0699591.

XX

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX

PI Busfield SJ, Gearing DP;

XX

DR WPI; 1998-169084/15.

DR

P-PSDB; AAW48379.

XX

PT Mouse and human don-1 polypeptide(s) - useful for treatment of
 PT melanomas and adenocarcinoma(s), and for wound healing

PS Claim 4; Fig 1; 121pp; English.

CC The sequence is that of a murine don-1 gene splice variant.
CC Don-1 polypeptides stimulate proliferation of epithelial cells
CC and thus are implicated in melanomas and adenocarcinomas in which
CC epithelial cells proliferate out of control. Compounds that
CC interfere with don-1 mediated cell proliferation can be used
CC in the treatment of tumours such as melanomas and adenocarcinomas
CC of the skin, oesophagus, lung, breast, liver, pancreas,
CC gastrointestinal tract, colon, prostate or uterus. Alternatively,
CC don-1 polypeptides can be used to stimulate epithelial cell
CC proliferation, e.g. for wound healing.

SQ Sequence 2467 BP; 592 A; 752 C; 706 G; 417 T; 0 other;

Query Match 44.8%; Score 402.2; DB 19; Length 2467;
Best Local Similarity 87.5%; Pred. No. 5.1e-84;
Matches 440; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

[illegible]

RESULT 15

ABS56034

ID ABS56034 standard; cDNA; 1561 BP.

XX

AC ABS56034;

XX

DT 14-JAN-2003 (first entry)

XX

DE cDNA encoding murine secreted splice variant of Don-1.

XX

KW Murine; Don-1; epidermal growth factor; EGF; neuregulin; mouse;
KW glycoprotein ligand; cell proliferation; cell proliferative disorder;
KW carcinoma; adenocarcinoma cell; myeloma; cell differentiation;
KW cell survival; epithelial cell; wound healing; tumour formation;
KW brain; vulnerary; cytostatic; gene therapy; chromosome 18; gene; ss.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT CDS

78..623

FT

/*tag= a

FT

/product= "Secreted splice variant of Don-1"

XX

PN US2002127594-A1.

XX

PD 12-SEP-2002.

XX

PF 12-MAR-2002; 2002US-0096241.

XX

PR 22-JUN-2000; 2000US-0599789.

XX

PA (GEAR/) GEARING D P.

PA

(BUSF/) BUSFIELD S J.

XX

PI Gearing DP, Busfield SJ;

XX

DR WPI; 2003-039584/03.

DR

P-PSDB; ABG71637.

XX

PT Novel Don-1 polypeptide useful for stimulating proliferation of cells,
PT for identifying proteins that interact with Don-1, and for regulating
PT tumour formation and progression in brain -

XX

PS Claim 4; Fig 2; 66pp; English.

XX

CC The present invention relates to the isolation of a novel gene
CC called Don-1, and alternate splice variants of Don-1, which are
CC related to epidermal growth factors (EGF) such as neuregulins.
CC Don-1 polypeptides are glycoprotein ligands. Both murine and human
CC Don-1 sequences are cloned. The mouse Don-1 gene maps to chromosome 18.
CC Don-1 polypeptides are useful for stimulating proliferation of a cell.
CC Antibodies to Don-1 polypeptides are useful for detecting Don-1
CC in a sample. The Don-1 polypeptides are useful for treating and
CC diagnosing cell proliferative disorders and play a role in the
CC proliferation of carcinomas e.g. adenocarcinoma, myeloma, in cell
CC differentiation, proliferation and survival. The polypeptides are
CC also useful for inhibiting proliferation of adenocarcinoma cells,

CC for stimulating the proliferation of cells such as epithelial cells
CC to promote wound healing, for identifying proteins that interact
CC with Don-1, and for regulating tumour formation and progression in
CC the brain. The polynucleotide sequences encoding Don-1 may be used
CC in gene therapy. The present sequence encodes murine secreted
CC splice variant of Don-1.
XX

SQ Sequence 1561 BP; 361 A; 479 C; 465 G; 256 T; 0 other;

Query Match 43.9%; Score 393.4; DB 25; Length 1561;
Best Local Similarity 87.7%; Pred. No. 5.1e-82;
Matches 441; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

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QY 371 CCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 430
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 CTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCA-CC 60
QY 431 GGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGA 490
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GGCCCAAGCTGAAGAAGATGAAGAGCCAGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCA 120
QY 491 AGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGG 550
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 AGTGTGAGGCAGCGCGGGAAACCCCGAGCCCTCCTATCGCTGGTTCAAGGATGGCAAGG 180
QY 551 AGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAACTCAGCAG 610
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 AACTCAACCGGAGTCGTGATATTTCGCATCAAGTATGGCAATGTCAGAAAGAACTCAGGCG 240
QY 611 TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA 670
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 TACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTACGTCTGTGAGGCCGAGAACA 300
QY 671 TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGT 730
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Db 301 TCCTTGGGAAGGACACCGTGAGGGGGCCGACTCCATGTCAACAGCGTGAGCACCACCTGT 360
QY 731 CATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATG 790
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 361 CATCCTGGTCGGGACATGCCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATG 420
QY 791 GAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGAT 850
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 421 GAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGAT 480
QY 851 ACACCGGGGACAGGTGTCAGCAG 873
    | | | | | | | | | | | | | | | | | |
Db 481 TCTTCGGACAGAGATGTTTGAG 503
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Search completed: January 14, 2004, 08:16:39
Job time : 292.304 secs

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 07:16:01 ; Search time 66.4093 Seconds
(without alignments)
5961.825 Million cell updates/sec

Title: US-09-864-675-3
Perfect score: 897
Sequence: 1 atgaggcgcgacccggcccc.....caatgggtcaacttctcctaa 897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	835.4	93.1	1884	3	US-08-753-007A-5	Sequence 5, Appli
2	835.4	93.1	1884	3	US-09-398-496-5	Sequence 5, Appli
3	784	87.4	3441	2	US-08-525-864A-1	Sequence 1, Appli
4	738.6	82.3	993	2	US-08-525-864A-3	Sequence 3, Appli
5	427.8	47.7	1476	3	US-08-753-007A-7	Sequence 7, Appli
6	427.8	47.7	1476	3	US-09-398-496-7	Sequence 7, Appli
7	427.8	47.7	2268	3	US-08-753-007A-31	Sequence 31, Appl
8	427.8	47.7	2268	3	US-09-398-496-31	Sequence 31, Appl
9	405.4	45.2	1607	3	US-08-753-007A-3	Sequence 3, Appli
10	405.4	45.2	1607	3	US-09-398-496-3	Sequence 3, Appli
11	405.4	45.2	2467	3	US-08-753-007A-1	Sequence 1, Appli

12	405.4	45.2	2467	3	US-09-398-496-1	Sequence 1, Appli
13	216.2	24.1	1207	2	US-08-525-864A-5	Sequence 5, Appli
14	84	9.4	2003	1	US-08-036-555B-21	Sequence 21, Appl
15	84	9.4	2003	1	US-08-469-569-21	Sequence 21, Appl
16	84	9.4	2003	1	US-08-249-322A-21	Sequence 21, Appl
17	84	9.4	2003	1	US-08-469-526A-21	Sequence 21, Appl
18	84	9.4	2003	2	US-08-734-591A-21	Sequence 21, Appl
19	84	9.4	2003	2	US-08-469-660-21	Sequence 21, Appl
20	84	9.4	2003	3	US-08-341-018-71	Sequence 71, Appl
21	84	9.4	2003	3	US-08-470-335-21	Sequence 21, Appl
22	84	9.4	2003	3	US-08-735-021-21	Sequence 21, Appl
23	84	9.4	2003	3	US-08-734-664A-21	Sequence 21, Appl
24	84	9.4	2003	3	US-08-470-339-21	Sequence 21, Appl
25	84	9.4	2003	4	US-08-467-602-21	Sequence 21, Appl
26	84	9.4	2003	5	PCT-US94-05083C-21	Sequence 21, Appl
27	84	9.4	2003	5	PCT-US95-06846A-21	Sequence 21, Appl
28	83.4	9.3	1108	1	US-08-036-555B-135	Sequence 135, App
29	83.4	9.3	1108	1	US-08-469-569-135	Sequence 135, App
30	83.4	9.3	1108	1	US-08-249-322A-135	Sequence 135, App
31	83.4	9.3	1108	1	US-08-469-526A-135	Sequence 135, App
32	83.4	9.3	1108	2	US-08-734-591A-135	Sequence 135, App
33	83.4	9.3	1108	2	US-08-469-660-135	Sequence 135, App
34	83.4	9.3	1108	3	US-08-341-018-5	Sequence 5, Appli
35	83.4	9.3	1108	3	US-08-470-335-135	Sequence 135, App
36	83.4	9.3	1108	3	US-08-735-021-135	Sequence 135, App
37	83.4	9.3	1108	3	US-08-734-664A-135	Sequence 135, App
38	83.4	9.3	1108	3	US-08-470-339-135	Sequence 135, App
39	83.4	9.3	1108	4	US-08-467-602-135	Sequence 135, App
40	83.4	9.3	1108	5	PCT-US94-05083C-131	Sequence 131, App
41	83.4	9.3	1108	5	PCT-US95-06846A-135	Sequence 135, App
42	78.4	8.7	1193	1	US-08-469-526A-134	Sequence 134, App
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44	78.4	8.7	1193	3	US-08-341-018-3	Sequence 3, Appli
45	78.4	8.7	1193	3	US-08-470-335-134	Sequence 134, App

ALIGNMENTS

RESULT 1

US-08-753-007A-5

; Sequence 5, Application US/08753007A

; Patent No. 6074841

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:


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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/753,007A
; FILING DATE: 19-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,591
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07334/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1884 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 664...1883
; OTHER INFORMATION:
US-08-753-007A-5

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Query Match          93.1%; Score 835.4; DB 3; Length 1884;
Best Local Similarity 98.1%; Pred. No. 8.6e-200;
Matches 856; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
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Db      218 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 277
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy      61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      278 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 337
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy      121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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Db      338 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 397
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy      181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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Db      398 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 457
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Qy      241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
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Db      458 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 517
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Qy      301 CGCTACATCTTTTCTGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360

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Db	518	CGCTACATCTTTTCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	577
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	578	CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC	636
Qy	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	637	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	696
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	697	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	756
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Db	757	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	816
Qy	601	AACTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	817	AACTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	876
Qy	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	877	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	936
Qy	721	ACCACCCTGTCATCCTGGTTCGGGGCAGCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	937	ACCACCCTGTCATCCTGGTTCGGGGCAGCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	996
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Db	997	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT	1056
Qy	841	CCTGTGGGATACACCGGGACAGGTGTCAGCAG	873
Db	1057	CCAAATGGATTCTTCGGACAGAGATGTTTGAG	1089

RESULT 2

US-09-398-496-5

; Sequence 5, Application US/09398496

; Patent No. 6133423

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

Db 458 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 517
 QY 301 CGCTACATCTTTTTCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
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 Db 518 CGCTACATCTTTTTCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 577
 QY 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
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 Db 578 CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC 636
 QY 421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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 Db 637 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 696
 QY 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
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 Db 697 CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 756
 QY 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 600
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 Db 757 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 816
 QY 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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 Db 817 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 876
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 Db 937 ACCACCCTGTCATCCTGGTTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 996
 QY 781 TCGGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
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 Db 997 TCGGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 1056
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 Db 1057 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 1089

RESULT 3

US-08-525-864A-1

; Sequence 1, Application US/08525864A

; Patent No. 5912326

; GENERAL INFORMATION:

; APPLICANT: Chang, Han

; TITLE OF INVENTION: Cerebellum-derived Growth Factors, and Uses

; TITLE OF INVENTION: Related thereto

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

```

; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AscII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,864A
; FILING DATE: 8-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: HUI-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3441 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 180..2441
US-08-525-864A-1

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Query Match          87.4%; Score 784; DB 2; Length 3441;
Best Local Similarity 92.2%; Pred. No. 7.5e-187;
Matches 826; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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QY      61 TACTCGCCAGCCTCAAGTCAGTGAGGACCGGTACAAGGCACCCGTGGTGGTGGAG 120
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Db      240 TACTCGCCAGCCTCAAGTCCGTGCAGGACCGGTACAAGGCACCCGTGGTGGTGGAG 299
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QY      121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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Db      300 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCAGCTCTAACAGCACCCGAGAGCCT 359
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QY      181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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Db      360 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 419
        |||||||||||||||||||||||||||||||||||||||||||||||||||
QY      241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
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Db      420 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 479
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QY      301 CGCTACATCTTTTTCTGGAGCCACCGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
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; FILING DATE: 19-NOV-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/699,591
 ; FILING DATE: 19-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fasse, J. Peter
 ; REGISTRATION NUMBER: 32,983
 ; REFERENCE/DOCKET NUMBER: 07334/022001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-542-5070
 ; TELEFAX: 617-542-8906
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1476 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 69...1475
 ; OTHER INFORMATION:
 US-08-753-007A-7

Query Match 47.7%; Score 427.8; DB 3; Length 1476;
 Best Local Similarity 89.8%; Pred. No. 6.9e-98;
 Matches 459; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy	363	CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG	422
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Qy	423	CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	482
Db			
	158	AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	217
Qy	483	ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	542
Db			
	218	ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	277
Qy	543	TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA	602
Db			
	278	TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA	337
Qy	603	CTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	662
Db			
	338	CTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	397
Qy	663	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	722
Db			
	398	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	457
Qy	723	CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG	782
Db			
	458	CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG	517

QY 783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
Db |||||||
518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577
QY 843 TGTGGGATAACCGGGGACAGGTGTCAGCAG 873
Db |||| | || | || || | ||
578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608

RESULT 6

US-09-398-496-7

; Sequence 7, Application US/09398496
; Patent No. 6133423

GENERAL INFORMATION:

APPLICANT: Gearing, David P.
APPLICANT: Buef...

APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION:

TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
AND USES THEREOF

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSER

ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin

CITY: Boston

CITY: Boston

STATE: MA

COUNTRY: US

COUNTRY: US
ZIP: 02110-2804
COMPUTER:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 3.31

OPERATING SYSTEM: DOS
SOFTWARE

SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION: FAST

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/398,496
FILING DATE:

FILING DATE:

CLASSIFICATION:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICANT:

APPLICATION NUMBER: 08/753,007

FILED DATE: 19-NOV-1996

APPLICATION NUMBER: 08/699,591
FILING DATE: 10/10/2008

FILING DATE: 19-AUG-1996
ATTORNEY/AGENT

ATTORNEY/AGENT INFORMATION:
NAME: E-

NAME: Fasse, J. Peter

REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET

REFERENCE/DOCKET NUMBER: 07334/022001

TELEPHONE: 617 540

TELEPHONE: 617-542-5070
TELEFAX: 617-542-5070

TELEFAX: 617-542-8906
TELE: 617-542-8906

TELEX:

FORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS

SEQUENCE CHARACTERISTICS:

LENGTH: 1476 base pairs
TYPE: nucleotide

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: linear
FEATURE: cDNA

FEATURE:

```

;      NAME/KEY:  Coding Sequence
;      LOCATION:  69...1475
;      OTHER INFORMATION:
US-09-398-496-7

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Query Match

Best Local Similarity 47.7%; Score 427.8; DB 3; Length 1476;
Matches 459; Conservative 89.8%; Pred. No. 6.9e-98;

Similarity 89.8%; Pred. No. 6.9e-98; Length 1476;
 Matches 459; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
 363 CCTCGATACCAACGGCA

Qy
Db

363 CCTCGATACCAACGGCAA^AAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422

98 CCGCGGCAAGAAGCACCCAGACCGG

Dd
98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCCGATCCCGGGGAGAA 157

Qy
423 CGCCACCCGGCCCAAGTTCAGGCTCCTCAAGAAAAGAGGTGGGCCAAGATCCTGTGCACTGACTG 422

QY 423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 157
Db 158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482

Dd
158 AGCCACCCGGCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482

Qy
483 ATCGCTGAAGTGTGAGCCAGCAGGACAGGTGGGTGAGAAGCA 217

QY 483 ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCCTACCGTTGGTTCAAGGA 217
Db 218 ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCCTACCGTTGGTTCAAGGA 542

Dbb
218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542

Qy
543 TGGCAAGGAGCTCAACGCCAAGGAA 277

QY 543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 277
Db 278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 602

Db
278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 602
Qy
603 CTCACGACTACAGTTCAACAACTTTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy 603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 337
Db 338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662

Db
338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
Qy
663 CGAGAACATCCTGGGGAACGAGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy 663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 397
Db 398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722

Db
398 CGAGAACATCCTGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
QY
723 CACCCTGTCATCCTGGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

QY 723 CACCCTGTCTCCTGGTCTGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 457

Db 458 CACCCTGTCTCCTGGTCTGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782

[illegible]

QY 783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 517
Db 518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842

Db
518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
Qy
843 TGTGGGATACACCGGGCAGCTCTCCTGCAAATGTCC 577

Qy 843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
Db 578 AAATGGATTCTTCGGACAGCAGT

Db 578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608

RESULT 7

US-08-753-007A-31

; Sequence 31, Application US/08753007A
; Patent No. 6074841

Patent No. 6074841
GENERAL INFORMATION:

APPLICANT: Gearing, David P.

APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION:

TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

Db 278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 337
 QY 603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
 Db 338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397
 QY 663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
 Db 398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457
 QY 723 CACCCTGTCATCCTGGTCCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
 Db 458 CACCCTGTCATCCTGGTCCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517
 QY 783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
 Db 518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577
 QY 843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
 Db 578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608

RESULT 8

US-09-398-496-31

; Sequence 31, Application US/09398496
; Patent No. 6133423

GENERAL INFORMATION:

APPLICANT: Gearing, David P.

APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

TITLE OF INVENTION: AND USES THEREFOR

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/398,496

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/753,007

FILING DATE: 19-NOV-1996

APPLICATION NUMBER: 08/699,591

FILING DATE: 19-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Fasse, J. Peter

REGISTRATION NUMBER: 32,983

RESULT 9

US-08-753-007A-3

; Sequence 3, Application US/08753007A
; Patent No. 6074841

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/753,007A
; FILING DATE: 19-NOV-1996
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/699,591
; FILING DATE: 19-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07334/022001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: Coding Sequence
; LOCATION: 79...621

; OTHER INFORMATION:

US-08-753-007A-3

Query Match

Best Local Similarity 45.2%; Score 405.4; DB 3; Length 1607;

Matches 442; Conservative 87.9%; Pred. No. 2.8e-92;

0; Mismatches 61; Indels 0; Gaps 0;

QY

371 CCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 430

Db 2 CTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 61
 QY 431 GGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGA 490
 Db 62 GGCCCAAGCTGAAGAAGATGAAGAGCCAGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCA 121
 QY 491 AGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGG 550
 Db 122 AGTGTGAGGCAGCGGGGAAACCCCCAGCCCTCCTATCGCTGGTTCAAGGATGGCAAGG 181
 QY 551 AGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGAC 610
 Db 182 AACTCAACCGGAGTCGTGATATTCGCATCAAGTATGGCAATGTGAGAAAGAACTCACGGC 241
 QY 611 TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA 670
 Db 242 TACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTACGTCTGTGAGGCCGAGAACA 301
 QY 671 TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGT 730
 Db 302 TCCTTGGGAAGGACACCGTGAGGGGCCGACTCCATGTCAACAGCGTGAGCACCCTCTGT 361
 QY 731 CATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATG 790
 Db 362 CATCCTGGTCGGGACATGCCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATG 421
 QY 791 GAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGAT 850
 Db 422 GAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGAT 481
 QY 851 ACACCGGGGACAGGTGTCAGCAG 873
 Db 482 TCTTCGGACAGAGATGTTTGGAG 504

RESULT 10

US-09-398-496-3

; Sequence 3, Application US/09398496

; Patent No. 6133423

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

Db	302	TCCTTG	GGAAGG	ACACCG	TGAGGG	GCCGAC	TCCATG	TCAACAG	CGTGAG	CACCACT	CTGT	361
QY	731	CATCCT	GGTCG	GGGCAC	GCCCCG	GAAGTG	CAACGAG	ACAGCCA	AGTCCT	ATTGCG	TCAATG	790
Db	362											
		CATCCT	GGTCG	GGGACAT	GCCCCG	GAAGTG	CAATGAG	ACCGCCA	AGTCCT	ACTGTG	TGAATG	421
QY	791	GAGGCG	TCTGCT	ACTACAT	CGAGGG	CATCAAC	CAGCTCT	CCTGCA	AGTGTCT	CCTGTG	GGGAT	850
Db	422											
		GAGGCG	TGTGCT	ACTACAT	CGAGGG	CATCAAC	CAGCTCT	CCTGCA	AATGTCC	AAACGG	AT	481
QY	851	ACACCG	GGGGAC	AGGTGT	CAGCAG							873
Db	482											
		TCTTCG	GACAG	AGATGT	TTTGAG							504

RESULT 11

US-08-753-007A-1

; Sequence 1, Application US/08753007A
; Patent N. 6,857,400

; Patent No. 6074841

; GENERAL INFORMATION:

APPLICANT: Gearing, David P.

APPLICANT: Busfield, Samantha J.

: TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
 : TITLE OF INVENTION:

; TITLE OF INVENTION: AND USES THEREFOR
 : NUMBER OF SHEETS

; NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/753,007A

FILING DATE: 19-NOV-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/699,591

FILING DATE: 19-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Fasse, J. Peter

REGISTRATION NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 07334/022001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2467 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

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;     TOPOLOGY:  circular
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  Coding Sequence
;       LOCATION:  79...1893
;       OTHER INFORMATION:
US-08-753-007A-1

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Query Match          45.2%;  Score 405.4;  DB 3;  Length 2467;
Best Local Similarity 87.9%;  Pred. No. 3.2e-92;
Matches 442;  Conservative 0;  Mismatches 61;  Indels 0;  Gaps 0;

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QY      371 CCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 430
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2   CTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 61

QY      431 GGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGA 490
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      62  GGCCCAAGCTGAAGAAGATGAAGAGCCAGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCA 121

QY      491 AGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGG 550
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      122 AGTGTGAGGCAGCGCGGGAAACCCCGAGCCCTCCTATCGCTGGTTCAAGGATGGCAAGG 181

QY      551 AGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGAC 610
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      182 AACTCAACCGGAGTCGTGATATTCGCATCAAGTATGGCAATGTCAGAAAGAACTCACGGC 241

QY      611 TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA 670
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      242 TACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTACGTCTGTGAGGCCGAGAACA 301

QY      671 TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGT 730
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      302 TCCTTGGGAAGGACACCGTGAGGGGGCCGACTCCATGTCAACAGCGTGAGCACCACCTCTGT 361

QY      731 CATCCTGGTCGGGGACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATG 790
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      362 CATCCTGGTCGGGACATGCCCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATG 421

QY      791 GAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGAT 850
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      422 GAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAATGTCCAAACGGAT 481

QY      851 ACACCGGGGACAGGTGTCAGCAG 873
          | | | | | | | | | | | | | | | | | |
Db      482 TCTTCGGACAGAGATGTTTGGAG 504

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RESULT 12

US-09-398-496-1

; Sequence 1, Application US/09398496

; Patent No. 6133423

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

```

; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/398,496
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/753,007
; FILING DATE: 19-NOV-1996
; APPLICATION NUMBER: 08/699,591
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07334/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2467 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 79...1893
; OTHER INFORMATION:
US-09-398-496-1

```

```

Query Match          45.2%; Score 405.4; DB 3; Length 2467;
Best Local Similarity 87.9%; Pred. No. 3.2e-92;
Matches 442; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

```

```

QY      371 CCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 430
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2   CTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 61

QY      431 GGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGA 490
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      62  GGCCCAAGCTGAAGAAGATGAAGAGCCAGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCA 121

QY      491 AGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGG 550

```

Db 122 AGTGTGAGGCAGCGGCGGGAAACCCCGAGCCCTCCTATCGCTGGTTCAAGGATGGCAAGG 181
 Qy 551 AGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGAC 610
 Db 182 AACTCAACCGGAGTCGTGATATTTCGCATCAAGTATGGCAATGTCAGAAAGAACTCACGGC 241
 Qy 611 TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA 670
 Db 242 TACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTACGTCTGTGAGGCCGAGAACA 301
 Qy 671 TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGT 730
 Db 302 TCCTTGGGAAGGACACCGTGAGGGGCCGACTCCATGTCAACAGCGTGAGCACCCTGT 361
 Qy 731 CATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATG 790
 Db 362 CATCCTGGTCGGGACATGCCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATG 421
 Qy 791 GAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGAT 850
 Db 422 GAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAATGTCCAACGGAT 481
 Qy 851 ACACCGGGGACAGGTGTGAGCAG 873
 Db 482 TCTTCGGACAGAGATGTTTGGAG 504

RESULT 13

US-08-525-864A-5

; Sequence 5, Application US/08525864A

; Patent No. 5912326

; GENERAL INFORMATION:

; APPLICANT: Chang, Han

; TITLE OF INVENTION: Cerebellum-derived Growth Factors, and Uses

; TITLE OF INVENTION: Related thereto

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: AscII (text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/525,864A

; FILING DATE: 8-SEP-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Kara, Catherine J.

; REGISTRATION NUMBER: 41,106

; REFERENCE/DOCKET NUMBER: HUI-017

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..394
US-08-525-864A-5

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Query Match          24.1%; Score 216.2; DB 2; Length 1207;
Best Local Similarity 86.3%; Pred. No. 5.4e-45;
Matches 239; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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QY      597 AAAGAACTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTG 656
      |||
Db      1 AAAGAACTCAGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTG 60
      |||
QY      657 CGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGT 716
      |||
Db      61 TGAGGCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGT 120
      |||
QY      717 GAGCACCACTCTGTCATCCTGGTTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTC 776
      |||
Db      121 GAGCACCACTCTGTCGTCCTGGTTCGGGGCAGCCCCGGAAGTGCAATGAGACAGCCAAGTC 180
      |||
QY      777 CTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAA 836
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RESULT 14

US-08-036-555B-21

; Sequence 21, Application US/08036555B

; Patent No. 5530109

; GENERAL INFORMATION:

; APPLICANT: Goodearl, Andrew; Stroobant, Paul;

; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;

; APPLICANT: Chen, Maio Su; Hiles, Ian

; TITLE OF INVENTION: Glial Mitogenic Factors, Their

; TITLE OF INVENTION: Preparation and Use

; NUMBER OF SEQUENCES: 184

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

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; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,555B
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2003
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: N in positions 31 and 32 could be either
; OTHER INFORMATION: A or G.
US-08-036-555B-21

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Query Match 9.4%; Score 84; DB 1; Length 2003;

Best Local Similarity 49.0%; Pred. No. 7.3e-12;

Matches 361; Conservative 0; Mismatches 345; Indels 30; Gaps 4;

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CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM
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 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,569
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/036,555
 FILING DATE: 24-MAR-1993
 APPLICATION NUMBER: 07/965,173
 FILING DATE: 23-OCT-1992
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 PRIOR APPLICATION DATA:
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 FILING DATE: 10-APRIL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Tsai, Christine H.
 REGISTRATION NUMBER: 34,266
 REFERENCE/DOCKET NUMBER: LUD 5250.4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2003
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
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 OTHER INFORMATION: N in positions 31 and 32 could be either
 OTHER INFORMATION: A or G.
 US-08-469-569-21

Query Match 9.4%; Score 84; DB 1; Length 2003;
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Db 822 GACCTGGGGCCACCCCGCCTTCCCTCCTGCGGGAGGCTCAAGGAGGACAGCAGGTACAT 881
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 Db 882 CTTCTTCATGGAGCCCGACGCCAACAGCACCAGCCGCGCGCCGCGCCCTTCCGAGCCTC 941
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 10:23:13 ; Search time 346.751 Seconds
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Title: US-09-864-675-3
Perfect score: 897
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	897	100.0	897	9	US-09-864-675-3	Sequence 3, Appli
	2	849	94.6	994	9	US-09-864-675-1	Sequence 1, Appli
	3	835.4	93.1	1884	14	US-10-096-241-5	Sequence 5, Appli
	4	427.8	47.7	1476	14	US-10-096-241-7	Sequence 7, Appli
	5	427.8	47.7	2268	14	US-10-096-241-31	Sequence 31, Appl
	6	405.4	45.2	1607	14	US-10-096-241-3	Sequence 3, Appli
	7	405.4	45.2	2467	14	US-10-096-241-1	Sequence 1, Appli
	8	173	19.3	201	13	US-10-029-386-26613	Sequence 26613, A
	9	173	19.3	573	13	US-10-029-386-12913	Sequence 12913, A
c	10	113.6	12.7	579	13	US-10-029-386-2532	Sequence 2532, Ap
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	12	84	9.4	1986	11	US-09-373-658-71	Sequence 71, Appl
	13	84	9.4	1986	12	US-09-989-687-71	Sequence 71, Appl
	14	84	9.4	2003	7	US-08-736-019-21	Sequence 21, Appl
	15	84	9.4	2003	11	US-09-366-886-71	Sequence 71, Appl
	16	84	9.4	2003	11	US-09-373-658-72	Sequence 72, Appl
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	18	83.4	9.3	1108	7	US-08-736-019-135	Sequence 135, App
	19	83.4	9.3	1108	11	US-09-366-886-5	Sequence 5, Appli
	20	78.4	8.7	1193	7	US-08-736-019-134	Sequence 134, App
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	22	76.8	8.6	1140	7	US-08-736-019-149	Sequence 149, App
	23	76.8	8.6	1140	11	US-09-366-886-55	Sequence 55, Appl
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	44	45.8	5.1	543	11	US-09-918-995-26620	Sequence 26620, A
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ALIGNMENTS

RESULT 1
 US-09-864-675-3
 ; Sequence 3, Application US/09864675
 ; Patent No. US20020081286A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Marchionni, Mark

; TITLE OF INVENTION: NRG-2 NUCLEIC ACID MOLECULES,
 ; TITLE OF INVENTION: POLYPEPTIDES, AND DIAGNOSTIC AND THERAPEUTIC METHODS
 ; FILE REFERENCE: 04585/049002
 ; CURRENT APPLICATION NUMBER: US/09/864,675
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/206,495
 ; PRIOR FILING DATE: 2000-05-23
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 897
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-864-675-3

Query Match 100.0%; Score 897; DB 9; Length 897;
 Best Local Similarity 100.0%; Pred. No. 5e-243;
 Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Qy	301	CGCTACATCTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
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Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
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Qy	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
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Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
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RESULT 2

US-09-864-675-1

; Sequence 1, Application US/09864675

; Patent No. US20020081286A1

; GENERAL INFORMATION:

; APPLICANT: Marchionni, Mark

; TITLE OF INVENTION: NRG-2 NUCLEIC ACID MOLECULES,

; TITLE OF INVENTION: POLYPEPTIDES, AND DIAGNOSTIC AND THERAPEUTIC METHODS

; FILE REFERENCE: 04585/049002

; CURRENT APPLICATION NUMBER: US/09/864,675

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/206,495

; PRIOR FILING DATE: 2000-05-23

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 994

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-864-675-1

Query Match 94.6%; Score 849; DB 9; Length 994;

Best Local Similarity 98.3%; Pred. No. 1.8e-229;

Matches 858; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
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        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
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Db	121		GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
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Qy	361		CCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
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US-10-096-241-5

; Sequence 5, Application US/10096241

; Publication No. US20020127594A1

; GENERAL INFORMATION:

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; APPLICANT: Gearing, David P.
; Busfield, Samantha J.
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; AND USES THEREFOR
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/096,241
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,591
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07334/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1884 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 664...1883
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-096-241-5

```

```

Query Match          93.1%; Score 835.4; DB 14; Length 1884;
Best Local Similarity 98.1%; Pred. No. 1.4e-225;
Matches 856; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

```

```

Qy      1 ATGAGGCGCGACCCGGCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      218 ATGAGGCGCGACCCGGCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 277

Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      278 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 337

```


Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	338	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	397
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	398	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	457
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	458	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	517
Qy	301	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	518	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	577
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	578	CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC	636
Qy	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	637	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	696
Qy	481	CAATCGCTGAAGTGTGAGGCGAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	697	CAATCGCTGAAGTGTGAGGCGAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	756
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG	600
Db	757	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG	816
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	817	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	876
Qy	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	877	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	936
Qy	721	ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	937	ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	996
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT	840
Db	997	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT	1056
Qy	841	CCTGTGGGATACACCGGGGACAGGTGTCAGCAG	873
Db	1057	CCAAATGGATTCTTCGGACAGAGATGTTTGGAG	1089

RESULT 4

US-10-096-241-7

; Sequence 7, Application US/10096241

```

; Publication No. US20020127594A1
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
;           Busfield, Samantha J.
; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
;                   AND USES THEREFOR
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/096,241
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,591
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07334/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1476 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 69...1475
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-096-241-7

```

```

Query Match          47.7%; Score 427.8; DB 14; Length 1476;
Best Local Similarity 89.8%; Pred. No. 1.4e-110;
Matches 459; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

```

```

Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
          || || | || | | | | ||| || | | || | | ||
Db      98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482

```

```

      |||
Db      158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217
Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
      |||
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277
Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 602
      |||
Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 337
Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
      |||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397
Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
      |||
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457
Qy      723 CACCCTGTCTATCCTGGTTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
      |||
Db      458 CACCCTGTCTATCCTGGTTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517
Qy      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
      |||
Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGGCATCAACCAGCTCTCCTGCAATGTCC 577
Qy      843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
      |||
Db      578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608

```

RESULT 5

US-10-096-241-31

; Sequence 31, Application US/10096241

; Publication No. US20020127594A1

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
; AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/096,241

; FILING DATE: 12-Mar-2002

```

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,591
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07334/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 69...2009
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-096-241-31

```

```

Query Match          47.7%; Score 427.8; DB 14; Length 2268;
Best Local Similarity 89.8%; Pred. No. 1.6e-110;
Matches 459; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

```

```

Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
        || || | || | | | | || | || | | ||
Db      98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
        |||||
Db      158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
        |||||
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 602
        |||||
Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
        |||||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
        |||||
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

Qy      723 CACCCTGTCATCCTGGTCTGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
        |||||
Db      458 CACCCTGTCATCCTGGTCTGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517

```

QY 783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
 |||
 Db 518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577
 QY 843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
 |||
 Db 578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608

RESULT 6

US-10-096-241-3

; Sequence 3, Application US/10096241

; Publication No. US20020127594A1

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
 ; AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/096,241

; FILING DATE: 12-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/699,591

; FILING DATE: 19-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Fasse, J. Peter

; REGISTRATION NUMBER: 32,983

; REFERENCE/DOCKET NUMBER: 07334/022001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1607 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 79...621

Db	182	AACTCAACCGGAGTCGTGATATTTCGCATCAAGTATGGCAATGTCTAGAAAGAACTCACGGC	241
Qy	611	TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA	670
Db	242	TACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTACGTCTGTGAGGCCGAGAACA	301
Qy	671	TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACTCTGT	730
Db	302	TCCTTGGGAAGGACACCGTGAGGGGCCGACTCCATGTCAACAGCGTGAGCACCACTCTGT	361
Qy	731	CATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATG	790
Db	362	CATCCTGGTTCGGGACATGCCCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATG	421
Qy	791	GAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGAT	850
Db	422	GAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGAT	481
Qy	851	ACACCGGGGACAGGTGTCAGCAG	873
Db	482	TCTTCGGACAGAGATGTTTGGAG	504

US-10-029-386-26613

; Sequence 26613, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

10; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES

USEFUL FOR GENE

; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

```

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

```

; SEO ID NO 26613

; LENGTH: 201

TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

: OTHER INFORMATION: MAP TO CHR5.3

```

: OTHER INFORMATION: EXPRESSED IN HEART. SIGNAL = 0.55

```

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.49

OTHER INFORMATION: EXPRESSED IN FETAL LIVER. SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN BRAIN. SIGNAL = 0.66

: OTHER INFORMATION: SWISSPROT HIT: Q14511 - EVALUATE 3.00e-29

```

: OTHER INFORMATION: NT HIT: AF119152.1. EVALUATE 1.00e-109

```

```

: OTHER INFORMATION: EST HUMAN HIT: BF108794.1. EVALUATE 3.00e-93

```

Query Match 19.3%; Score 173; DB 13; Length 201;

Best Local Similarity 100.0%; Pred. No. 6.9e-39;


```

Qy      424 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 483
          |||
Db      27  GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 86

Qy      484 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 543
          |||
Db      87  TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 146

Qy      544 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAG 596
          |||
Db      147 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAG 199

```

RESULT 9

US-10-029-386-12913

; Sequence 12913, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE

; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 12913

; LENGTH: 573

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO CHR5.3

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.55

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.49

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.66

; OTHER INFORMATION: SWISSPROT HIT: O14511, EVALUE 2.00e-28

; OTHER INFORMATION: NT HIT: AF119152.1, EVALUE 0.00e+00

; OTHER INFORMATION: EST_HUMAN HIT: BG996653.1, EVALUE 1.00e-108

US-10-029-386-12913

Query Match 19.3%; Score 173; DB 13; Length 573;

Best Local Similarity 100.0%; Pred. No. 8.9e-39;

Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      424 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 483
          |||
Db      377 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 436

Qy      484 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 543
          |||
Db      437 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 496

```

Qy 544 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAG 596
 |||
 Db 497 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAG 549

RESULT 10

US-10-029-386-2532/c

; Sequence 2532, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
 USEFUL FOR GENE

; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 2532

; LENGTH: 579

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO CHR5.1

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.5

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.3

; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.2

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6

; OTHER INFORMATION: NT HIT: AF119153.1, EVALUE 0.00e+00

; OTHER INFORMATION: EST_HUMAN HIT: BF108794.1, EVALUE 2.00e-57

; OTHER INFORMATION: SWISSPROT HIT: O14511, EVALUE 2.00e-12

US-10-029-386-2532

Query Match 12.7%; Score 113.6; DB 13; Length 579;

Best Local Similarity 92.9%; Pred. No. 5.1e-22;

Matches 130; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 594 CAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGT 653
 |||

Db 489 CAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGT 430

Qy 654 CTGCGAGGCCGAGAACATCCTGGGGAAGGACACCG-TCCGGGGCCGGCTTTACGTCAACA 712
 |||

Db 429 CTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGCTCCGGGGCCGGCTTTACGTCAACA 370

Qy 713 GCGTGAGCACCACCCTGTCA 732
 ||| || ||| |||

Db 369 GCGGTAGGTGGGCCCAGACA 350

RESULT 11


```
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 1986
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Unknown
US-09-373-658-71
```

```
Query Match          9.4%; Score 84; DB 11; Length 1986;
Best Local Similarity 49.0%; Pred. No. 1.6e-13;
Matches 361; Conservative 0; Mismatches 345; Indels 30; Gaps 4;
```

```
Qy      189 GGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGGGGGCTGCA 248
      || ||| || | | || ||| ||| | | ||| |||
Db      759 GGTGTGGGCGGTGAAAGCCGGGGGCTTGAAGAAGGACTCGCTGCTCACCGTGCGCCTGGG 818

Qy      249 GCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAGCGCTACAT 308
      | | | | | | | | | | | | | | | | | | | | | |
Db      819 GACCTGGGGCCACCCCGCCTTCCCCTCCTGCGGGAGGCTCAAGGAGGACAGCAGGTACAT 878

Qy      309 CTTTTTCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACG-----GCCTT 356
      ||| ||| ||| ||| ||| | | | | | | | | | | | |
Db      879 CTTCTTCATGGAGCCCAGCCCAACAGCACCAGCCGCGCGCCGGCCGCTTCCGAGCCTC 938

Qy      357 TGCCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCAC 416
      | |||| | ||| || ||| ||| ||| ||| ||| ||| |||
Db      939 TTTCCCCCCTCTGGAGACGGGCCGGAACCTCAAGAAGGAGGTGAGCCGGGTGCTGTGCAA 998

Qy      417 TGA CTGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGA 476
      ||||| | ||| | |||| ||||| ||||| ||||| | |||
Db      999 GCGGTGCGCCTTGCCCTCCCCAATTGAAAGAGATGAAAAGCCAGGAATCGGCTGCAGGTT 1058

Qy      477 GAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTT 536
      || | | || ||||| | | | | | | | | | | | |
Db      1059 CAAACTAGTCCTTCGGTGTGAAACCAGTTCTGAATACTCCTCTCTCAGATTCAAGTGGTT 1118

Qy      537 CAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCA---TCAAATATGGCAACGG 593
      |||| |||| || || | || || | | | | | | ||| ||
Db      1119 CAAGAATGGGAATGAATTGAATCGAAAAACAAACCACAAAATATCAAGATACAAAAAA 1178

Qy      594 CAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGT 653
      | ||| ||| ||| | | |||| | ||| || |||| ||||| |
Db      1179 GCCAGGGAAGTCAGAACTTCGCATTAACAAAGCATCACTGGCTGATTCTGGAGAGTATAT 1238

Qy      654 CTGCGAGGCCGAGAACATCCTGGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAG 713
      ||| | | | || | || || |||| | | | | | |
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Db 1239 GTGCAAAGTGATCAGCAAATTAGGAAATGACAGTGCCTCTGCCAATATCACCATCGTGGA 1298
 Qy 714 CGTGAGCACCACCCTGTCATCC-----TGGTCGGGGGCACGCCCAGGAAGTGCAACGAGAC 767
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1299 ATCAAACGCTACATCTACATCCACCACTGGGACAAGCCATCTTGTAATAATGTGCGGAGAA 1358
 Qy 768 AGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCT 827
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1359 GGAGAAAACCTTTCTGTGTGAATGGAGGGGAGTGCCTTCATGGTGAAAGACCTTTCAAACCC 1418
 Qy 828 CTC-----CTGCAAAGTGTCCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGC 878
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1419 CTCGAGATACTTGTGCAAAGTGCCCAAATGAGTTTACTGGTGATCGCTGCCAAAACCTACGT 1478
 Qy 879 AATGGTCAACTTCTCC 894
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1479 AATGGCCAGCTTCTAC 1494

RESULT 13

US-09-989-687-71

; Sequence 71, Application US/09989687

; Publication No. US20040002449A1

; GENERAL INFORMATION:

; APPLICANT: Hastings, Gregg A.

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides

; FILE REFERENCE: 1488.107000D

; CURRENT APPLICATION NUMBER: US/09/989,687

; CURRENT FILING DATE: 2001-11-21

; NUMBER OF SEQ ID NOS: 126

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 71

; LENGTH: 1986

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism:Unknown

US-09-989-687-71

Query Match 9.4%; Score 84; DB 12; Length 1986;

Best Local Similarity 49.0%; Pred. No. 1.6e-13;

Matches 361; Conservative 0; Mismatches 345; Indels 30; Gaps 4;

Qy 189 GGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGCCGCTCCGGAGCGGGGGGCTGCA 248
 | | | | | | | | | | | | | | | | | | | | | |
 Db 759 GGTGTGGGCGGTGAAAGCCGGGGGCTTGAAGAAGGACTCGCTGCTACCGTGCGCCTGGG 818
 Qy 249 GCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAGCGCTACAT 308
 | | | | | | | | | | | | | | | | | | | | | |
 Db 819 GACCTGGGGCCACCCCGCCTTCCCCTCCTGCGGGAGGCTCAAGGAGGACAGCAGGTACAT 878
 Qy 309 CTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACG-----GCCTT 356
 | | | | | | | | | | | | | | | | | | | | | |
 Db 879 CTTCTTCATGGAGCCCAGGCCAACAGCACCAGCCGCGCGCCGGCCGCTTCCGAGCCTC 938
 Qy 357 TGCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCAC 416

Db 939 TTTCCCCCCTCTGGAGACGGGCCGGAACCTCAAGAAGGAGGTCAGCCGGGTGCTGTGCAA 998
 Qy 417 TGA CTGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGA 476
 Db 999 GCGGTGCGCCTTGCCTCCCCAATTGAAAGAGATGAAAAGCCAGGAATCGGCTGCAGGTTC 1058
 Qy 477 GAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCTACCGTTGGTT 536
 Db 1059 CAACTAGTCCTTCGGTGTGAAACCAGTTCTGAATACTCTCTCAGATTCAAGTGGTT 1118
 Qy 537 CAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCA---TCAAATATGGCAACGG 593
 Db 1119 CAAGAATGGGAATGAATTGAATCGAAAAACAAACCACAAAATATCAAGATACAAAAAA 1178
 Qy 594 CAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGT 653
 Db 1179 GCCAGGGAAGTCAGAACTTCGCATTAACAAAGCATCACTGGCTGATTCTGGAGAGTATAT 1238
 Qy 654 CTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAG 713
 Db 1239 GTGCAAAGTGATCAGCAAATTAGGAAATGACAGTGCCTCTGCCAATATCACCATCGTGA 1298
 Qy 714 CGTGAGCACCACCCTGTCATCC-----TGGTCGGGGCACGCCCCGGAAGTGCAACGAGAC 767
 Db 1299 ATCAAACGCTACATCTACATCCACCACTGGGACAAGCCATCTTGTAATAATGTGCGGAGAA 1358
 Qy 768 AGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCT 827
 Db 1359 GGAGAAAACCTTCTGTGTGAATGGAGGGGAGTGCTTCATGGTGAAAGACCTTTCAAACCC 1418
 Qy 828 CTC-----CTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTTCGC 878
 Db 1419 CTCGAGATACTTGTGCAAGTGCCCAAATGAGTTTACTGGTGATCGCTGCCAAAACCTACGT 1478
 Qy 879 AATGGTCAACTTCTCC 894
 Db 1479 AATGGCCAGCTTCTAC 1494

RESULT 14

US-08-736-019-21

; Sequence 21, Application US/08736019

; Publication No. US20030207799A1

; GENERAL INFORMATION:

; APPLICANT: Goodearl, Andrew

; APPLICANT: Stroobant, Paul

; APPLICANT: Minghetti, Luisa

; APPLICANT: Waterfield, Michael

; APPLICANT: Marchionni, Mark

; APPLICANT: Chen, Mario

; APPLICANT: Hiles, Ian

; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR

; TITLE OF INVENTION: PREPARATION AND USE

; NUMBER OF SEQUENCES: 189

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Clark & Elbing LLP

```

; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/736,019
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,833
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2003
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: N in positions 31 and 32 could be
; OTHER INFORMATION: either A or G.
US-08-736-019-21

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Query Match          9.4%; Score 84; DB 7; Length 2003;
Best Local Similarity 49.0%; Pred. No. 1.6e-13;
Matches 361; Conservative 0; Mismatches 345; Indels 30; Gaps 4;

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Qy 189 GGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGGGGGCTGCA 248
 || ||| || | | || || | ||| ||| | | | | |||
 Db 762 GGTGTGGGCGGTGAAAGCCGGGGGCTTGAAGAAGGACTCGCTGCTCACCGTGCGCCTGGG 821

Qy 249 GCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACAGCGCTACAT 308
 | | | | | | | | | | | | | | | | | | | | | |
 Db 822 GACCTGGGGCCACCCCGCTTCCCCTCCTGCGGGAGGCTCAAGGAGGACAGCAGGTACAT 881

Qy 309 CTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACG-----GCCTT 356
 ||| ||| ||| ||| | | | | | | | | | | | | | |
 Db 882 CTTCTTCATGGAGCCCGACGCCAACAGCACCAGCCGCGCGCCGGCCGCTTCCGAGCCTC 941

Qy 357 TGCCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCAC 416
 | |||| | ||| || ||||| |||| | | |||||
 Db 942 TTTCCCCCTCTGGAGACGGGCCGGAACCTCAAGAAGGAGGTGAGCCGGGTGCTGTGCAA 1001

Qy 417 TGAAGTGCAGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGA 476
 ||||| | ||| ||||| ||||| ||||| | |||
 Db 1002 GCGGTGCGCCTTGCTTCCCAATTGAAAGAGATGAAAGCCAGGAATCGGCTGCAGGTTC 1061

Qy 477 GAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGAATCCCCAGCCTTCTACCGTTGGTT 536
 || | | || ||||| | | | | | | | | |||||
 Db 1062 CAACTAGTCCTTCGGTGTGAAACCAGTTCTGAATACTCCTCTCTCAGATTCAAGTGGTT 1121

Qy 537 CAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGA---TCAAATATGGCAACGG 593
 |||| |||| || || | || || | | | | |||| ||
 Db 1122 CAAGAATGGGAATGAATTGAATCGAAAAACAAACCACAAAATATCAAGATACAAAAAA 1181

Qy 594 CAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGT 653
 | ||| ||| ||| ||| || ||||| || || ||||| |||||
 Db 1182 GCCAGGGAAGTCAGAACTTCGCATTAACAAAGCATCACTGGCTGATTCTGGAGAGTATAT 1241

Qy 654 CTGCGAGGCCGAGAATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAG 713
 ||| | | | || | || || || || || | | | | |||
 Db 1242 GTGCAAAGTGATCAGCAAATTAGGAAATGACAGTGCCTCTGCCAATATCACCATCGTGGA 1301

Qy 714 CGTGAGCACCACCCTGTCATCC-----TGGTCGGGGCACGCCCAGGAGTGAACGAGAC 767
 | | | | ||||| || | | || ||||| |||||
 Db 1302 ATCAAACGCTACATCTACATCCACCACTGGGACAAGCCATCTTGTAATGTGCGGAGAA 1361

Qy 768 AGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCT 827
 | || | | || ||||| | |||| | | | | | |
 Db 1362 GGAGAAAACCTTCTGTGTGAATGGAGGGGAGTGCTTCATGGTGAAAGACCTTCAAACCC 1421

Qy 828 CTC-----CTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGC 878
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 Db 1422 CTCGAGATACTTGTGCAAGTGCCCAAATGAGTTTACTGGTGATCGCTGCCAAAACCTACGT 1481

Qy 879 AATGGTCAACTTCTCC 894
 |||| | |||| |
 Db 1482 AATGGCCAGCTTCTAC 1497


```

; Publication No. US20030040465A1
; GENERAL INFORMATION:
; APPLICANT: Gywnne, David I.
; APPLICANT: Mahanthappa, Nagesh K.
; APPLICANT: Marchionni, Mark A.
; APPLICANT: Bermingham-McDonogh, Olivia
; APPLICANT: Goldin, Stanley M.
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: USE OF NEUREGULINS AS MODULATORS OF
; TITLE OF INVENTION: CELLULAR COMMUNICATION
; FILE REFERENCE: 04585/041005
; CURRENT APPLICATION NUMBER: US/09/366,886
; CURRENT FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: US 08/341,018
; PRIOR FILING DATE: 1994-11-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 2003
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (265)...(1530)
; NAME/KEY: variation
; LOCATION: (31)...(32)
; OTHER INFORMATION: n can be a or g.
US-09-366-886-71

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Query Match          9.4%; Score 84; DB 11; Length 2003;
Best Local Similarity 49.0%; Pred. No. 1.6e-13;
Matches 361; Conservative 0; Mismatches 345; Indels 30; Gaps 4;

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Qy      189 GGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGGGGGCTGCA 248
      ||  ||| || |  |  ||  || | |||  |||| | | || | |||
Db      762 GGTGTGGGCGGTGAAAGCCGGGGGCTTGAAGAAGGACTCGCTGCTCACCCTGCGCCTGGG 821

Qy      249 GCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAGCGCTACAT 308
      | | |  |  | | | |||| | | |||| | | | | |||||
Db      822 GACCTGGGGCCACCCCGCCTTCCCCTCCTGCGGGAGGCTCAAGGAGGACAGCAGGTACAT 881

Qy      309 CTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACG-----GCCTT 356
      ||| ||| ||||| || |  |  |  |  |  |  |  |||
Db      882 CTTCTTCATGGAGCCCAGCCAACAGCACCAGCCGCGCGCCGGCCGCCTTCCGAGCCTC 941

Qy      357 TGCCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCAC 416
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Db      942 TTTCCCCCTCTGGAGACGGGCCGAACCTCAAGAAGGAGGTGAGCCGGGTGCTGTGCAA 1001

Qy      417 TGA CTGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGA 476
      |||||  |  ||| | |||| | |||| | |||| |  |||
Db      1002 GCGGTGCGCCTTGCCCTCCCAATTGAAAGAGATGAAAAGCCAGGAATCGGCTGCAGGTTT 1061

Qy      477 GAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTT 536
      || | |  || ||||| |  |  |  |  |  |  |  |||
Db      1062 CAAACTAGTCCTTCGGTGTGAAACCAGTTCTGAATACTCCTCTCTCAGATTCAAGTGGTT 1121

```

